

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

Friday, June 09, 2006

Case Serial Number: 09/743825

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Davis,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

Thursday, May 04, 2006

Case Serial Number: 09/743825

From: Noble Jarrell

Location: Biotech-Chem Library

Rem 1B71

Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes	





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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

.rapbm (Published_Applications_AA_New).

THE TOP BONK USC.

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession This Page Blank Juspto

7.3.6.28

STIC-Biotech/ChemLib

187401

ME

From:

Chan, Christina

Sent:

Thursday, April 27, 2006 10:52 AM

To:

Davis, Minh-Tam; STIC-Biotech/ChemLib

Subject:

RE: Rush search request for 09/743825

Please with Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Thursday, April 27, 2006 10:15 AM

To:

Chan, Christina

Subject:

Rush search request for 09/743825

Please search for interference only:

1) SEQ ID NO:1.

2) Nucleotides 77-1753 of SEQ ID NO:1.

3) SEQ ID NO: 7, 8 and 10, with size limitation for the data in the database to the size of the corresponding sequences.

THANK YOU

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

,

Ţyp	e of Search
NA# <u>Υ</u>	AA#:
S/L:	Oligomer:
Encode/Tr	ansl:
Structure #	t:Text:
Inventor:	Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: Campuger
WWW/Internet:
Other (Specify):

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73622

STIC-Biotech/ChemLib

192 242

MG

From:

Chan, Christina

Sent:

Wednesday, June 07, 2006 1:36 PM

To: Subject: Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/743825

Please Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644

(571)-272-0841

Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, June 07, 2006 1:32 PM

To:

Chan, Christina

Subject:

Rush search request for 09/743825

Please search in commercial database, issued patent files and PGPUB:

SEQ ID NO:7, 8, 10 with size limitation for the sequences in the database to the size of the corresponding sequences.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA# AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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9, 2006, 00:36:21 ; Search time 289 Seconds (without alignments) 482.509 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                         June
                                                                                                                                         Run on:
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5244920 seqs, 3486124231 residues US-09-743-825-10 20 1 gaccgcatagacttctcaga 20 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Scoring table: Sequence: Searched:

2681012 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001as:*
geneseqn2001bs:*
geneseqn2002as:*
geneseqn2003as:*
geneseqn2003as:*
geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2005s:* geneseqn2006s:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* N_Geneseq_8:* 101 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTTANATIO

		Description	Aaz50446 Human PB3	Aax93486 PCR prime	Aad62200 Human hae	Aee31152 Haemophil	Adt00440 Novel mut	Adw95798 Human TFR	Adz44776 Human tra	Aca08287 Necrosis	Aca06680 NFKB sub-	Aaz48549 Human TNF	Abt05045 TNFR1 exp	Adr06077 Human TNF	Adg73193 Pseudomon	Adl12249 Pseudomon	Adi79866 Mouse HMG	Adi79673 Mouse HMG	Adw95797 Human TFR	Adx57319 Forward P
SUMMAKIES		ΩI	AAZ50446	AAX93486	D AAD62200	5 AEE31152	3 ADT00440	1 ADW95798	4 ADZ44776	ACA08287	ACA06680	AAZ48549	ABT05045	3 ADR06077	D ADG73193) ADL12249	2 ADI79866	2 ADI79673	1 ADW95797	4 ADX57319
		Match Length DB	20 3	20 2	20 1(19 1	20 1:	20 1	20	17 8	17 8	18 3	18 6	18 13	19 1(19 1(20	20 1;	20 17	20 14
,	*	Match I	100.0	69.0	0.99	63.0	63.0	63.0	63.0	62.0	62.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0
		Score	20	13.8	13.2	12.6	12.6	12.6	12.6	12.4	12.4	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2
	1	No.	-	7	с С	Ω 4	S	9	7	œ	6	c 10	c 11	c 12	13	14	15	c 16	17	18

Add244775 Human tra Add27863 Primer pa Aa221763 Exemplary Aac60963 TATA box- Add262063 TATA box- Add262063 TATA box- Add262063 TATA box- Add27631 Human cyt Aav30475 Canine be Aec47021 Antisense Aec47074 Antisense Add7751 Human AdG Add7751 Human ACA Aec11754 Human ACA Aec11754 Human ACA Aec11754 Human ACA Aec11361 Human ACA Aec50761 Hu	
ADZ44775 AAQ32840 AAQ32840 AAQ32840 AAQ51863 AAD51763 AD148431 AAC476315 AAC47617 AEC47621 AE	
1000001100011111100011444400011111000	
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ALIGNMENTS

PB39; human; prostate cancer; PC; chromosome llpll.1-11.2; cancer; prostate epithellum; splicing mechanism; early diagnosis; progression; precancerous cell; metastatic potential; non-neoplastic prostate disease; expressed sequence tag; EST; PCR primer; ss. Human PB39 specific 3' RACE primer. AAZ50446 standard; DNA; 20 BP. 99WO-US016831. 98US-0094137P 18-MAY-2000 (first entry) WO200005376-A1. Homo sapiens. 23-JUL-1999; 24-JUL-1998; 03-FEB-2000. AAZ50446; AAZ50446

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Chuaqui RF, Cole KA, Liotta LA;

WPI; 2000-182700/16.

cancer.

Claim 5; Page 18; 51pp; English.

Novel gene which is dysregulated in prostate cancer useful for diagnosing

The present sequence is the human PB39 3' specific RACE primer, from EST clone AAR00504. It is used to determine the complete nucleotide sequence of PB39 cDNA, isolated from human pancreas cDNA library using RACE. The PB39 gene that is dysregulated in prostate cancer has homology to the EST AAR00504. PB39 gene is located on chromosome 11p11.1-11.2. Abnormally

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high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema frames of the C. pneumoniae genome (see AAX345819 can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences can also be used as immunogenic compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                  Score 20; DB 3; Length 20;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                               Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                           differing aggressiveness and metastatic potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 1595; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                         GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                        1 GACCGCATAGACTTCTCAGA
                                                                                                                                                                                                    100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97FR-00014673,
98US-0107078P,
                                                                                                                                                                                                                                                                                                                                                                                                AAX93486 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydophila pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-357842/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1997;
04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX93486;
                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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The invention relates to a compound targetted to a nucleic acid molecule encoding haematopoietic cell protein tyrosine kinase. The compound inhibits the expression of haematopoietic cell protein tyrosine kinase and it specifically hybridises with the nucleic acid molecule encoding the tyrosine kinase or with at least an 8-nucleobase portion of an active site on the nucleic acid molecule encoding the tyrosine kinase. The antisense compounds are useful for modulating the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoletic cell protein tyrosine kinase and treating diseases or conditions associated with the expression of the tyrosine kinase, such as hyperpoliferative disorders (e.g. cancer), inflammation, diabetes or a viral infection. The antisense compounds are also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in
                                                                                                                                                                                                                                                 Haematopoietic cell; tyrosine kinase; hyperproliferative disorder; cancer; therapy; inflammation; diabetes; viral infection; inflammation; tumour; cytostatic; virucide; antisense therapy; antisense; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorothioate backbone; All cytidines are 5-methyl cytidines"
                                                                                                                                                                                                                  Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides targeted to nucleic acids encoding hematopoietic cell protein tyrosine kinase, useful for diagnosing treating cancer (e.g. leukemia), inflammation, diabetes or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "2'-0-methoxyethyl (2'-MOB) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "2'-0-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Page 26; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                       phosphorothioate backbone; ss.
                      3 GACCGCATAAACTTATC 19
 GACCGCATAGACTTCTC 17
                                                                                                                AAD62200 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2001; 2001US-00007010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2001; 2001US-00007010.
                                                                                                                                                                                  15-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-811000/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003125275-A1
                                                                                                                                                                                                                                                                                                                                                                                                   modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                   AAD62200;
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                                                                                                 AAD62200/
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Gaps

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69.0%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 2.7e+03; ive 0; Mismatches 2; Indels

15; Conservative

Best Local Similarity Matches 15; Conserv

Query Match

(4) making (M2)

AEE31211, AEE31241, AEE31246, AEE31263 and AEE31231;

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Fri Jun

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The invention relates to an isolated polypeptide (I) critical for the survival of Haemophilus sp. comprising an amino acid sequence having at least 95% structural similarity with an amino acid sequence chosen from AEE31317, AEE313132, AEE31345, AEE31353, AEE31354 and AEE31317, AEE313130, AEE31345, AEE31345, AEE31354 and EAE31358. Also described: (I) an isolated polynucleotide (II) critical for the survival of Haemophilus sp. comprising a nucleotide sequence having at least 95% structural similarity with nucleotide sequence chosen for a coding sequence in AEE31062, AEE31130, AEE31140, AEE31155, AEE31156, and AEE31241, AEE31241, AEE31241, AEE31241, AEE31241, AEE31241, AEE31241, AEE31241, AEE31346, and a sequence comprising a nucleotide sequence chosen from AEE31062, AEE31130, AEE311310, AEE31331, AEE31331, AEE31331, AEE31332, AEE31333, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polypeptide critical for survival of Haemophilus species, useful for reducing virulence of H. influenzae to be used as vaccine
                                                                                                                                                                                               Gaps
distinguishing between functions of various members of a biological pathway. The present sequence is human haematopoietic cell tyrosine kinase antisense oligonucleotide
                                                                                                                                                                                                  ö
                                                                                                                                                  Length 20;
                                                                                                                                                                                               Indels
                                                                                                                                             66.0%; Score 13.2; DB 10; 83.3%; Pred. No. 5.7e+03;
                                                                                              Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; antibacterial; trxB; PCR; primer; ss.
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 121; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae trxB PCR primer.
                                                                                                                                                                                             .
                                                                                                                                                                                                                                            2 ACCGCATAGACTTCTCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arvidson
                                                                                                                                                                                                                                                                     20 AACTCATTGACTTCTCAG 3
                                                                                                                                                                                                                                                                                                                                                                                       .152/c
ABE31152 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-2001; 2001US-0345438P.
21-OCT-2002; 2002US-00274586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2005; 2005US-00194246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-2006 (first entry)
                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2006-037204/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREP/) MOTT J E. (TREP/) TREPOD C M. (ARVI/) ARVIDSON S.
                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005272089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEE31152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mott JB,
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 4
AEE31152/ID AEE3
    ន្តដ្ឋមន្ត្
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          H. influenzae with reduced virulence, which involves altering a coding sequence in an H. influenzae to comprise a mutation, the non-mutagenized ocoding sequence comprising a nucleocide sequence chosen from RES1062, AEE31130, AEE31140, AEE31141, AEE31241, AEE31241, AEE31243 and AEE31231, and determining if the H. influenzae comprising the mutation the mutation compared to an H. influenzae comprising the comprise the mutation, (5) an H. influenzae obtained by (M2) and (6) a vaccine composition comprising the H. influenzae. (1) is useful for reducing the decreasing the growth rate of a microorganism. The present sequence represents a PCR primer for a H. influenzae trxB coding sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity actimulators. The invention may be useful for developing methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
tumourigensis; somatic alteration; colorectal cancer; NTRK3; FES;
GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
guanylate cyclase stimulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) as associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel mutant protein tyrosine kinase-related oligonucleotide SeqID428
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Velculescu V, Kinzler KW, Vogelstein B;
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                                                                                                                                                                                                                                                                                                                            63.0%; Score 12.6; DB 15; Length 19; 78.9%; Pred. No. 1.2e+04; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                     Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 428; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            2 ACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 ACCGCTTACACTTTCACA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT00440 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                               Local Similarity 78.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bardelli A, Parsons W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-718702/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT00440;
                                                                                                                                                                                                                                                                                                                            Query Match
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Diagnosing hereditary hemochromatosis, involves providing sample comprising patient's nucleic acid, detecting presence or absence of A424G allele of polymorphism in nucleic acid that encodes transferrin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and treatment of iron misregulation diseases including HFB bolypeptides and the polynucleotides encoding them. The iron misregulation diseases include both iron overload diseases and iron deficiency diseases. The invention is useful for diagnosing hereditary hemochromatosis and in gene therapy. The present sequence is human transferrin receptor (TFR) cDNA 424A allelle specific biotin-labeled oligonucleotide. This oligonucleotide is used in the screening for A424G polymorphism in the hereditary hemochromatosis patient chromosomes.
detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a human-derived oligonucleotide which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; pharmaceutical; iron overload; toxicity; intoxication; disorder of iron metabolism; hemochromatosis; cardiant; hepatotrophic; metabolic disorder; gene therapy; TFR; transferrin receptor; ss.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                            Human TFR cDNA 424A allele specific biotin-labeled 5' oligo, TFRdl.G
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                                                                                                                                  ·
0
                                                                                                    Length 20;
                                                                                                                                    Indels
                                                                                                / Match 63.0%; Score 12.6; DB 13; Local Similarity 78.9%; Pred. No. 1.2e+04; He 15; Conservative 0; Mismatches 4;
                                                                  Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/mod_base= OTHER
                                                                                                                                                                  1 GACCGCATAGACTICTCAG 19
                                                                                                                                                                                       GACCCCGTAGTCATCTCAG 20
                                                                                                                                                                                                                                                                                BP.
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97US-00834497.
97US-00866211.
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                                                                                                                                                                                                                                                                             ADW95798 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                              (first entry)
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modified_base
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04-APR-1997;
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                                                                                                  Query Match
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                                                                                                                                Matches
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63.0%; Score 12.6; DB 14; Length 20; 78.9%; Pred. No. 1.2e+04;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of treating hemochromatosis in a patient by administering the hemochromatosis protein HFB (HLA-H) to the patient. The method is used for treating hemochromatosis. The invention provides a molecular basis for the relationship of HFB to iron metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of hemochromatosis in a patient involves administering HFE (HLA
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                               Human transferrin receptor OLA oligonucleotide TFRd1.G SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and diagnostic and therapeutic agents for the treatment of iron misregulation diseases. The present sequence represents an oligonucleotide listation assay (OLA) oligonucleotide for the human transferin receptor, which is used in an example from the present
                                                                                                                                                                                                                         cardiant; hepatotropic; transferrin receptor; ss.
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  Indels
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Pred. No. 1.2e+04;
0; Mismatches 4;
  4.
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 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; SEQ ID NO 12; 26pp; English
                           GACCGCATAGACTTCTCAG 19
                                                  2 GACAGCACACTTCACCG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -H) polypeptide to the patient.
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97US-00866211.
97US-00920559.
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78.9%;
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                                                                                                                   ADZ44776 standard; DNA; 20
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                                                                                                                                                                    14-JUL-2005 (first entry
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Best Local Similarity 78.9
Matches 15, Conservative
 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIRA ) BIO-RAD LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-331970/34.
                                                                                                                                                                                                                         hemochromatosis;
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13-JUN-1997;
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                                                                                                                                                                                                                                                                Synthetic.
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Matches
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ID ACA(
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AC ACA(
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DT 03-5
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Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; Zinzyme; G-Cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer; prostate cancer; colorectal cancer; brain cancer; esophageal cancer; stomach cancer; brain cancer; cesophageal cancer; bromach cancer; brain cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glloma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methortexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gencitabine; radiation therapy; inflammatory disease; asthma; diabetes; restenosis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic alrway inflammation; inflammatory bowel disease; infection; ss.

Synthetic.

US2002177568-A1.

28-NOV-2002

23-MAY-2001; 2001US-00864785

92US-00987132. 94US-00245466. 94US-00291932. 96US-00777916. 18-MAY-1994; 23-DEC-1996; 07-DEC-1992;

(STIN/) STINCHCOMB D T.

. . (DRAP/) DRAPER K G. MCSWIGGEN

Draper KG; Mcswiggen J, Stinchcomb DT,

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 46; 72pp; English.

regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat configuration. The enzymatic nucleic acid molecule is adapted to treat configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methorizexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatese, diabetes, obseity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury septicion, graft molecules are also useful for treating inflammatory bowel disease or centerial nervous system (CNS) and mycocardial) glopesty, autoimmune disease, lupus, maltiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury septience or acid used to a necrosis factor kappa B sub-unit The invention describes an enzymatic nucleic acid molecule (I) which down

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG'2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung,

prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapises such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic

Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

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62.0%; Score 12.4; DB 8; Length 17; 64.3%; Pred. No. 1.5e+04; ive 4; Mismatches 1; Indels
               llarity 64.3%;
Conservative
             Local Similarity
les 9; Conserv
Query Match
Best Local S:
Matches 9,
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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                                                                               Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; d-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; broincare; brain cancer; colorectal cancer; brain cancer; cervical cancer; stomach cancer; bladder cancer; pancreatic cancer; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxal; docetaxal; cisplatin; methotrexate; chemotherapy; paclitaxal; docetaxal; cisplatin; edatexate; gencitabine; radiation therapy; inflammatory disease; asthma; diabetes; gencitabine; radiation therapy; inflammatory disease; obsity; ischaemia; gene therapy; autoimmune disease; Crohn's disease; obsity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic alrway inflammatory bowel disease; infection; ss.
                                                                                                                                                                                       NFKB sub-unit modulating inozyme substrate #499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draper KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 34; 72pp; English
                                                                                                   ACA06680 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-00987132.
94US-00245466.
94US-00291932.
96US-00777916.
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                CAUGGACTUCTICAG 17
CATAGACTTCTCAG 19
                                                                                                                                                          03-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                               ACA06680;
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use compound; tumour necrosis factor receptor 1; liver disease; hepatitis; liver injury; hyperproliferative disorder; cancer;

Antisense compound;

human; ds.

TNFR1;

22-OCT-2001; 2001WO-US051224.

WO200248168-A1. Homo sapiens.

20-JUN-2002

TNFR1 expression modulation related antisense oligo SEQ ID No 75.

(first entry)

11-0CT-2002

ABT05045;

BP

ABT05045 standard; DNA; 18

CGCCCAGTCTTCTCAGA

18

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides antisense compounds targeted to human tumour necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNFR1 human cells or tissues. The antisense compounds specifically hybridize with one or more nucleic acids encoding TNFR1 modulating the function of nucleic acid moderness encoding TNFR1, ultimately modulating the amount of TNFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. Sequences AAZ48482-565 represent antisense oligos used for inhibition of the human TNFR1 mRNA
acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or inflection. This sequence represents the substrate of a novel enzymatic
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
inflammation; tumour formation; TNFR1; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense inhibition of tumor necrosis factor type 1 expression for diagnosis, treatment and prevention of disease, particularly tumors.
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                                                                                                                                                                                                 Score 12.4; DB 8; Length 17;
Pred. No. 1.5e+04;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18942.
                                                                                                                                                              Sequence 17 BP; 4 A; 6 C; 3 G; 0 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10; Col 25; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                h 62.0%;
Similarity 64.3%;
9; Conservative
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                                                                                                                                                                                                                                                                        6 CATAGACTICICAG 19
                                                                                                                                                                                                                                                                                        2 CAUGGACUUCUCAG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.
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                                                                                                                           nucleic acid molecule
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ48549;
                                                                                                                                                                                                                                                                                                                                                                             AAZ48549/c
                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antisense compound targeted to nucleic acid molecule encoding tumor necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length targeted to nucleic acid molecule encoding tumour necrosis factor receptor 1 (TMFR1), where the antisense compound inhibities expression of TMFR1. The antisense compound is useful for inhibiting the expression of TMFR1 in cells or tissues. The antisense compound is also useful for treating an animal (preferably human) having a disease or condition associated with TMFR1, e.g. a liver disease (such as hepatitis, or liver the expression of TMFR1. The antisense compound is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. This polymucleotide sequence represents a human oligonucleotide relating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antisense compound 8 to 30 nucleotides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 12.2; DB 6; Length 18; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TNFR1 antisense oligonucleotide segid 75.
                                                                                                                                                                                                                                                                                                                                                                       Dean NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 45; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the TNFR1 of the invention
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                                                                                                                                                                                                                                                                                                         24-OCT-2000; 2000US-00695451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR06077 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Baker BF, Cowsert LM,
                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-583481/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-2004
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ID ADR0,
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XX DT 21-0
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Gaps

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61.0%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels

4 CGCATAGACTTCTCAGA 20

8

14; Conservative

Query Match Best Local Similarity Matches 14; Conserv

us-09-743-825-10.rng

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cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 (TANG/)
                                                                                                                                                                                                                                                                                                                                                     COLL/)
                                                                                                                                                                                                                                                                                                                                                                                           CART/)
                                                                                                                                                                                                                                                                                                                                                                                                                 SCHIN/)
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110 ADL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting radiation-induced apoptosis in a cell or tissue comprises administering to the cell or tissue an antisense oligonucleotide targeted to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a method of inhibiting radiation-induced apoptosis in a cell or tissue comprising administering to the cell or tissue an antisense oligonucleotide of 8-30 nucleotides in length targeted to a nucleic acid molecule encoding tumour necrosis factor receptor 1 (TNPR1). The method and antisense oligonucleotides are useful for inhibiting radiation-induced apoptosis in a cell or tissue, and for treating diseases associated with the expression of TNPR1. This sequence
                cytostatic; gene therapy; apoptosis inhibitor;
radiation-induced apoptosis; tumour necrosis factor receptor 1; INFR1;
human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a human tumour necrosis factor receptor 1 (INFR1) antisense oligonucleotide.
                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                     /note= "OTHER= Optionally 2'-0-Methoxyethyl (2'-MOB)
nucleotides"
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                                                                                                                                                                                                              'note= "OTHER= Phosphorothioate backbone"
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Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; SEQ ID NO 75; 24pp; English.
                                                                                                                                  cocation/Qualifiers
                                                                                                                                                                                            mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                   base= OTHER
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17-JUN-1999; 99WO-US013763.
24-OCT-2000; 2000US-00695451.
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il Similarity 82.4%;
14; Conservative
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                                                                                                                                                                                                                                                  *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004147471-A1
                                                                                                                                  Key
modified_base
                                                                                                                                                                                                                                                                                                                             modified base
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                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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New nucleic acid, useful in imparting disease resistance to a plant or in preparing a composition for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of Pseudomonas syringae pv. tomato DC3000 Avr/Hop proteins, and the polynucleotide sequences encoding them. Also disclosed are expression vectors, host cells, and transgenic plants comprising polynucleotide sequences of the invention. The polynucleotide and polypeptide sequences are useful in imparting disease resistance to a plant or in preparing a composition for treating cancer. The sequences may also be used to make a plant hypersusceptible to colonisation by nonpathogenic bacterial modify a metabolic pathway in a cell, cause enkaryotic cell death, and inhibit programmed cell death. The present sequence represents a PCR primer used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                            Avr; Hop; transgenic plant; disease resistance; cancer; bacteria; metabolic pathway; eukaryotic cell death; programmed cell death;
Pseudomonas syringae pv. tomato DC3000 Hop gene PCR primer #40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cartinhour SW, Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; Avr; Hop; cancer; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.2; DB 10;
Pred. No. 1.9e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas syringae anti-cancer gene primer #60.
                                                                                                                                                                                      Pseudomonas syringae; pv. tomato str. DC3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; SEQ ID NO 187; 209pp; English
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                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2003; 2003US-00365742.
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2002; 2002US-0356408P.
10-MAY-2002; 2002US-0380185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%;
                                                                                                                            cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALFANO J R.
CARTINHOUR S W.
SCHNEIDER D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collmer A, Alfano JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-875735/81.
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                                                                                                                                                                                                                                                US2003204868-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMG-COA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compounds, particularly antisense oligonucleotides targeted to
nucleic acid encoding HMG-CoA reductase, useful for treating
atherosclerosis, or a disease involving cholesterol metabolism or
                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule, useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 389
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0
                                                                                                                                                                                                                                                                                                      Tang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 12.2; DB 10; Length 19; ilarity 82.4%; Pred. No. 1.9e+04; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                      Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 187; 284pp; English.
                                                                                                                                                                                                                                                                                                      Cartinhour SW,
                                                                                                                                                                                       (USDA ) US SEC OF AGRIC.
(UYNE-) UNIV NEBRASKA.
(UNIV ) UNIV KANSAS STATE RES FOUND.
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                              12-FEB-2003; 2003WO-US004450.
                                                                                                                                                              CORR ) CORNELL RES FOUND INC
                                                                                12-FEB-2002; 2002US-0356408P.
10-MAY-2002; 2002US-0380185P.
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                                                                                                                                                                                                                                                                                                Collmer A, Alfano JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dean NM, Freier SM,
                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-679632/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-081743/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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AC AD17
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                                                                   The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylglutaryl-Consyme A (HMG-CoA) reductase, and inhibits the expression of HMG-CoA reductase. The novel compounds have cardiant, antiarteriosclerotic, and antilipaemic activities. The compound can be used to treat disorders by antisense gene therapy. The compounds compositions and methods are useful for treating a disease or condition associated with HMG-CoA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-CoA reductase. This polynucleotide sequence represents an antisense oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 12.2; DB 12; Length 20; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Example 16; SEQ ID NO 389; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9, 2006, 00:41:31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June
Job time : 293 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
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Adv65807 Sense str Add71043 Anti-FRK Ad179541 Human HWG Ad179738 Human HWG AC149676 HAVCR1 si AC149851 HAVCR1 si AC149851 HAVCR1 ta AC149851 HAVCR1 ta AC149851 HAVCR1 ta AC149851 HAWCR1 ta AC149851 HAWCR1 ta AC149851 Human MDZ AC1707 Human Shi Adb62331 Human IRA Adv87053 Human IRA Adv87053 Human PPA Adx03575 Antisense Adp68748 Human PPA Adx03575 Antisense Adf97151 Human Gen Adp68748 Human PPA Adx03575 Antisense Adf97151 Human Gen Adp68748 Human PPA Adx03575 Antisense Adf97151 Human Gen Adf96876 Bull Human HWB Ady6876 Human RPA Adx03575 Antisense Adf96876 Human RPA Adx03575 Antisense Adg6876 Human RPA Adx03575 Antisense Adg6876 Bull Human RPA Adx03575 Antisense Adg6876 Bull Human RPA Adx03575 Antisense Adg6876 Bull Human RPA

ADV65807 ADQ61043 ADI79738 ADI79738 ACL498676 ACL498678 ACL498678 ACL498678 AAV23903 AAV2701711 AAV27053 AAV296753 AAV296753 AAV296753 AAV296753 AAV3767053 AAV3767053 AAV3767053 AAV376753 AAV376753 AAV376753 AAV376753 AAV376753 AAV376753 AAV376753 AAV37575 AAV376754 AAV376754

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GenCore version 5.1.9 ucleic - nucleic search, using sw model on: June 8, 2006, 23:02:12; Search time 289 Seconds (without alignments) 506.634 Million cell updates/sec 1 ctggcgtatctgaagagtctg 21 ing table: IDENTITY NUC Gapop 10.0, Gapext 1.0 ched: 5244920 seqs, 3486124231 residues 1 number of hits satisfying chosen parameters: 3050480 num DB seq length: 0 mum DB seq length: 21 -processing: Minimum Match 100* Insting first 45 summaries N Genesqui990s:* 1: genesqui900s:* 3: genesqui200as:* 5: genesqui200as:* 6: genesqui200as:* 6: genesqui200as:* 7: genesqui200as:* 8: genesqui200as:* 10: genesqui200as:* 11: genesqui200as:* 12: genesqui200as:* 13: genesqui200as:* 14: genesqui200as:* 15: genesqui200as:* 16: genesqui200as:* 17: genesqui200as:* 18: genesqui200as:* 19: genesqui200as:* 10: genesqui200as:* 11: genesqui200as:* 12: genesqui200as:* 13: genesqui200as:* 14: genesqui200as:* 15: genesqui200as:* 16: genesqui200as:* 17: genesqui200as:* 18: genesqui200as:* 18: genesqui200as:* 19: genesqui200as:* 10: genesqui200as:* 11: genesqui200as:* 12: genesqui200as:* 13: genesqui200as:* 14: genesqui200as:* 15: genesqui200as:* 16: genesqui200as:* 17: genesqui200as:* 18: genesqui200as:* 18: genesqui200as:* 18: genesqui200as:*										* * H * * * * * * * * * * * * * * * * *	
OM n Run Titli Perfe Searr Total Minin Maxin Post-	GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.	leic - nucleic search, using sw mode	8, 2006, 23:02:12 ; S	Title: US-09-743-825-8 Perfect score: 21 Sequence: 1 ctggcgtatctgaagagtctg 21	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 5244920 seqs, 3486124231 residues	Total number of hits satisfying chosen parameters: 3050480	Minimum DB seq length: 0 Maximum DB seq length: 21	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	តិច្ចស្ថិត្តស្នេស	to: geneaeque

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaz50445 EST R0050	Adu41462 Knock-dow	Adj85951 Nucleic a	Aaz05689 PCR prime	Aec30315 Human loc	Aac63691 Rat P2X 7	Ada09833 Antisense	Aav97668 Human EGF	Adj85562 Nucleic a	Adk96254 Primer of	Adf50105 Human BCL	Adf50117 Human BCL	Adf50125 Human BCL	Adf50109 Human BCL	Adg29696 BCL2-tard	Adq29693 BCL2-tard	Adg29700 BCL2-targ	Adv65888 Antisense
SUMMARIES		ΩI	AAZ50445	ADU41462	ADJ85951	AAZ05689	AEC30315	AAC63691	ADA09833	AAV97668	ADJ85562	ADK96254	ADF50105	ADF50117	ADF50125	ADF50109	ADG29696	ADG29693	ADG29700	ADV65888
		Match Length DB	21 3	21 13	20 12	20 2	20 14	20 4	20 9	17 2	20 12	20 12	21 10	21 10	21 10	21 10	21 10	21 10	21 10	21 14
d	Query	Match L	100.0	66.7	65.7	64.8	62.9	61.9	61.9	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0
		Score	21	14	13.8	13.6	13.2	13	13	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8
	Result	No.	-	0	c o	Ω	0	9	7	80 U	0	10	11	c 15	c 13	c 14	15	c 16	c 17	c 18

ALIGNMENTS	RESULT 1 AAZ50445 ID AAZ50445 standard; DNA; 21 BP.	XX AC AAZ50445;	XX DT 18-MAY-2000 (first entry)	XX DE EST R00504-specific primer 2.	XX PB39; human; prostate cancer; PC; chromosome llp11.1-11.2; cancer;	w problede epithelium; spliching mednanism; early diagnosis; progression; KW precancerous cell; metastatic potential; non-neoplastic prostate disease; KW expressed sequence tag; EST; PCR primer; ss.	AAA. Homo sapiens.	XX PN WO200005376-A1.	XX PD 03-FEB-2000.	XX PF 23-JUL-1999; 99WO-US016831.	XX PR 24-JUL-1998; 98US-0094137P.	XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.	AA PI Chuaqui RF, Cole KA, Liotta LA; vv	DR WPI; 2000-182700/16.	PT Novel gene which is dysregulated in prostate cancer useful for diagnosing by cancer.	AA. PS Claim 5; Page 16; 51pp; English.	CA The present sequence is the BST AAR00504-specific PCR primer, used for CC amplification of sequences contained within the BST AAR00504. It is C useful to probe the gene overexpressed in prostate cancer epithelium and CC to analyse the differential expression of the BST. The PB39 gene that is CC dysregulated in prostate cancer is isolated from human pancreas CDNA
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Nucleic acid analysis-related Tag probe SeqID1019.
                                          ADJ85951 standard; DNA; 20 BP
                                                                                          06-MAY-2004 (first entry)
                                                                   ADJ85951;
                               ADJ85951/c
                    RESULT 3
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library and has homology to the EST AAR00504. PB39 gene is located on chromosome llpli.1-11.2. Abnormally high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of differing aggressiveness and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polynucleotide comprising an RNA sequence. The polynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.
                                                                                                                                                                                         Gaps
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                                                                                                                                                               Score 21; DB 3; Length 21; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 14; DB 13; Length 21; 100.0%; Pred. No. 3.3e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  ds; RNA production; protein production; drug development;
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesic
                                                                                                                                      Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clasen RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                             ch 100.0%; Score 21; DB 1 Similarity 100.0%; Pred. No. 0.8 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 6678; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Djokic K,
                                                                                                                                                                                                                1 CTGGCGTATCTGAAGAGTCTG 21
                                                                                                                                                                                                                               Knock-down target sequence #6641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GALA-) GALAPAGOS GENOMICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003; 2003WO-EP004362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2003; 2003WO-EP004362
                                                                                                                                                                                                                                                                                                   ADU41462 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VSCH/) VAN DER SCHUEREN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arts GJF, Lambrecht MJY,
Griffioen S, Bergs CJL;
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                 metastatic potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-775940/76.
                                                                                                                                                                            Local Similarity
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               knock-down target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004094636-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                  27-JAN-2005
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                                                                                                                                                                                                                                                                                                                           ADU41462;
                                                                                                                                                               Query Match
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Matches
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ADU41462/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA molecules made by annealing and extending overlapping 60mer oligonuclectides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
restriction endonuclease site; T3 promoter site; Tag gene; Poly A site; T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product validation; quality control; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.7%; Score 13.8; DB 12;
88.2%; Pred. No. 4.1e+03;
ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 1019; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                           14-JUL-2003; 2003WO-US021990.
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                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-2002; 2002US-0395530P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ05689/c
ID AAZ05689 standard; DNA; 20
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-122923/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christians FC;
                                                                                                                                                 Synthetic.
Unidentified.
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Gaps

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TGGCGTATCTGAAG 15

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Conservative

16 TGGCGTATCTGAAG 3

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                              Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (See AAZ01425). These ORFs encode polypeptides (See AAX36754-X37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, pendumitis, cervicitis, salpingttis, perihepatitis, bartholinitis, pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP; major histocompatibility complex; MHC; HLA; human leukocyte antigen; immune disorder; inflammation; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes; diabetes mellitus; myasthenia gravis; vitiligo; Graves disease; Hashimotos disease; Addison's disease; gastritis; autoimmune hepatitis; rheumatism; systemic lupus erythematosus; scleroderma; polymyositis; dermatomyositis; permicious anemia; primary biliary cirrhosis; idiopathic thrombocytopenia purpura; Sjoegrens syndrome; multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 5.2e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human locus-specific oligonucleotide #1603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 1791; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TGGCGTATCTGAAGAGTCTG 21
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97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 64.8%;
1 Similarity 80.0%;
16; Conservative (
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                                                                                                                                                                                                                                   Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-371125/31
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Best Local Similarity
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                                                                                                                                                                                                                                                                                             W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1997;
04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2005
                                                                                                                                                                                                                                                                                                                                                               10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffais R;
                                                                                                                                                                                                Synthetic.
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ID AEC3033
XA AC AEC3033
XX IT-NOV.
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The invention relates to a method of identifying the nucleotide for each of a set of single nucleotide polymorphisms (SNPs) in the major of a set of single nucleotide polymorphisms (SNPs) in the major comprising to comprising the HLA type for the individuals and identifying an SNP haplotype in the population that correlates with the HLA type, where the SNP haplotype in the population that correlates with the HLA type, where the SNP haplotype comprises the SNPs in the MHC region. The invention can she relates to a method of predicting the HLA type of an individual, a method of determining the presence or absence of an individual, a correlates with susceptibility to a disease or condition, and a method of determining the susceptibility of an individual to a disease or condition. The disease or condition is an immune disorder or inflammatory condition selected from inflammatory bowel disease, ulcerative colitis, crowls a disease, rheumatoid arthritis, diabetes, diabetes mellitus, myssthemia gravis, vitiligo, Graves disease, Hashimoto's disease, Crohn's disease, systemic selectosis, polymositis, dermatomyositis, opermicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia processors and proce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; muscular-gen.; neuroprotective; dermatological; antithyroid; hepatotropic; antianemic; hemostatic; ophthalmological; uropathic; antipsoriatic; ss; SNP detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying single nucleotide polymorphism (SNP) haplotype that correlates with the HLA type, useful for diagnosing an immunological inflammatory condition, comprises providing SNPs in the major histocompatability complex region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.2; DB 14; Length 20;
Pred. No. 8.4e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 6335; 175pp; English.
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                                                                                                                                                                                                                                                                                                     28-FEB-2005; 2005WO-US006628.
                                                                                                                                                                                                                                                                                                                                                       26-FEB-2004; 2004US-0547823P.
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2001 (first entry)
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oliphant A, Murray S;
                                                                                                                                                                                                                                                                                                                                                                                                         (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-638856/65.
                                                                                                                                                                                                    WO2005082110-A2.
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                      09-SEP-2005
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  EXEXEXEX
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antiarthritic; antibacterial; antiviral; antiallergic; cytostatic; cardiant; cerebroprotective; immunosuppressive; P2Z; purinergic receptor; nervous system disorder; chronic inflammation; Alzheimer's disease; rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection; haematopoietic system disorder; immune response; autoimmune disorder; allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; ss; primer; permeabilising activity; P2X7 receptor; P2Z receptor; receptor; ATP; antigen presenting cell; T lymphocyte; mitogenic stimulation; multinucleated giant cell; adenosine triphosphate; 3'-0-(4-benzoyl) benzoyl ATP; BAXTP; fluorescent dye; propidium iodide; nootropic; neuroprotective; immunosuppressive; cerebroprotective; vasocropic; arthritic disorder; respiratory disorder; neurodegenerative disease; Alzheimer's disease; inflammation; rheumatoid arthritis; amyloidosis; infection; tuberculosis; haematopoietic system; immune response; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.9%; Score 13; DB 4; Length 20; 100.0%; Pred. No. 1.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. w. ...
                                                                                                                                                                                                                                                                                                                                                                                                               Surprenant A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Col 7-8; 40pp; English.
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                                                                                                                                                                                                                                                                                         97US-00842079.
                                                                                                                                                                                                                                                                                                                               97US-00842079
                                                                                                                         tuberculosis; PCR primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                               Kawashima E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-006153/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                       28-APR-1997;
                                                                                                                                                                                                                                                                                                                             28-APR-1997;
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                                                                                                                                                                                                       US6133434-A
                                                                                                                                                                                                                                             17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodīes.
                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                             Buell GN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA09833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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  MARKAR AREXET STATES
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and the preterror uncumpliance monitoring when the and compound for its and electable molecule, preferably a fluorescent dye (e.g. propidium iodide). The inventive method is useful for screening a compound for its ability to modulate the permeabilishing activity of a mammalian P2X7 receptor useful for treatment of arthritic and respiratory disorders and neurodegenerative disease. It is particularly useful in the treatment of Albaimer's disease, diseases involving acute or chronic inflammation including rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, e.g. tuberculosis, disorders of the haematopoietic system and immune response, including autoimmune disorders, allergies and lymphoproliferative disorders diseases involving apoptotic cell death, such as cardiac and cerebral ischaemia. The sequence presented is a
                                                                                                                                                                                                                                                                                                                                                                Screening of compound for its ability to modulate permeabilizing activity of mammalian receptor useful for treating e.g. arthritis, and alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a method for screening a compound for its ability receptor. The P2Z receptor is a cell surface receptor for ATP and has been implicated in the lysis of antigen presenting cells by cytotoxic T lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well as in the formation of multinucleated giant cells. The preferred agonist is adenosine triphosphate (ATP) or 3,-0-(4-benzoyl)benzoyl ATP (BZATP) and the preferred method comprises monitoring the uptake into the cell of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, epidermal growth factor receptor; EGPR, EGP-R, target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nested PCR primer used for the amplification of rat P2X7 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
lymphoproliferative disorder; apoptosis; ischaemia, rat;
autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human EGF-R target sequence nucleotide position 3858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ....
                                                                                                                                                                                                                                                                                      Kawashima E;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 3; 43pp; English.
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                                                                                                                                                                       15-AUG-2000; 2000US-00638857.
                                                                                                                                                                                                            97US-00842079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTATCTGAAG 15
                                                                                                                                                                                                                                                                                    Buell GN, Surprenant A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 13; Conservative
                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                        WPI; 2003-502654/47.
                                                                                                                                                                                                              28-APR-1997;
                                                                                           JS6509163-B1
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                                                                                                                                 21-JAN-2003
                                                     Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                       disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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WO9833893-A2

06-AUG-1998

14-JAN-1998; 31-JAN-1997; 04-DEC-1997;

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This invention relates to a novel DNA molecule which comprises a DNA molecule made up of the following elements in a 5' to 3' direction: a first restriction endonuclease site; a T3 promoters site; at least one Tag gene comprising at least 5 20mer Tag sequences; a Poly A site having at least 21 consecutive A residues; a second restriction endonuclease site which may be the same or different than the first restriction endonuclease site; or a T7 Promoter on the opposite strand as the T3 promoter. The invention may be useful in nucleic acid analysis, in particular to synthetic Tag genes useful as assay controls, in assay development product development and validation and for quality control. The present sequence is that of a Tag oligonucleotide probe which may be used during the creation of the novel DNA molecule of the invention.
                                                                                                                    New DNA molecules made by annealing and extending overlapping 60mer oligonuclectides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide useful for PCR amplification along with two fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 12.8; DB 12; Length 20; 87.5%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 630; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GCGTATCTGAAGAGTC 19
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                                                          WPI; 2004-122923/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2003259875-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98866 to V9978 represent hammenhead ribozymes and hairpin ribozymes respectively for human EGF-R. The NAMS are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of EGF-R RNA in a cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         knzymatic nucleic acids - which cleave RNA derived from an epidermal
growth factor receptor, useful for inhibiting cell proliferation and for
treating cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 77; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Mcswiggen JA
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ID ADJUBS562 standard; DNA; 20 BP. XX
AC ADJUBS562;
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C ADJUBS562;
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C ADJUBS562;
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DE Nucleic acid analysis-related TaXX
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TO Fromoter; nucleic acid analys
XM restriction endomuclease site; T
XM assay development; product 
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                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC
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Matches 14; Conservative
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Query Match

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                                                                                                                                                                                                                                                                                                                                               88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
                                                                     Gaps
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                                Query Match 61.0%; Score 12.8; DB 12; Length 20; Best Local Similarity 87.5%; Pred. No. 1.3e+04;
                                                                    Indels
Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  Human BCL2 siNA target sequence SEQ ID NO:833.
                                                                  0; Mismatches
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2002US-0386782P.
2002US-0396905P.
2002US-0406784P.
2002US-0406784P.
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29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0408293P.
15-JAN-2003; 2003US-0440129P.
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                                                                                                                                                                                                                 ADF50105 standard; RNA; 21
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                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                  1 CTGGCGTATCTGAAGA
                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-712622/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003070969-A2.
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11-MAR-2002;
06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                 12-FEB-2004
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                                                                  Matchee
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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A sulf of the invention has cytostatic, immunosuppression, vircide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacognomics, studying gene function and gene mapping (e.g. of single-nuclecotide polymorphisms). The sequences shown in ADF49273-ADF50143
                                                                                                                                                                                                                                                                                                                                                                                                                                                88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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                                                                                                                                                                                                                                                                                                                                                                                           Human BCL2 siNA target sequence SEQ ID NO:845.
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18-UUL-2002; 2002US-0386905P.

29-AUG-2002; 2002US-0406784P.

09-SEP-2002; 2002US-0408378P.

09-SEP-2002; 2002US-040923P.

15-UAN-2003; 2003US-0440129P.
                                                                                                                                                                                                          ADF50117 standard; RNA; 21 BP
                        | : : | : | | | | | : | : | 4 GUCUCUGAAGACUCUG 19
   21
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GTATCTGAAGAGTCTG
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nes 14; Conservative
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06-JUN-2002;
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Matches
                                                                                                                                                     RESULT 12
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RESULT 13

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61.0%; Score 12.8; DB 10; Length 21; 56.2%; Pred. No. 1.4e+04; ive 5; Mismatches 2; Indels C

Query Match
Best Local Similarity 56.2
Matches 9; Conservative

us-09-743-825-8.rng

12-FEB-2004

ADF50125;

28-AUG-2003

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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNa of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to expression or activity be BCL2 by RNA interference. siNA are used to organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143 represent siNA of the invention.
                                                                     ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded short interfering nucleic acid; siNA; antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.0%; Score 12.8; DB 10; Length 21; 87.5%; Pred. No. 1.4e+04; vative 0; Mismatches 2; Indels 0
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                                 Human BCL2 siNA target sequence SEQ ID NO:837.
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2002US-0386782P.
2002US-0396905P.
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2002US-0408378P.
2002US-0409293P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J, Beigelman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG29696 standard; RNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the BCL2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2002;
05-SEP-2002;
09-SEP-2002;
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                            11-MAR-2002;
                                                                                                                                                                                                                                                                                                                                     20-FEB-2002;
                                                                                                                                                                                                                                                  28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA her useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. SiNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, pharmacogenomics, studying gene function and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single represent siNA of the invention.
                                                                                                                                                                                            88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
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                                                                                                                                                    Human BCL2 siNA target sequence SEQ ID NO:853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; SEQ ID NO 853; 148pp; English.
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11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0366782P.
18-JUL-2002; 2002US-0396905P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-04092378P.
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ADF50125/c
ID ADF50125 standard; RNA; 21
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                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcswiggen J, Beigelman L;
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Gaps

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12-FEB-2004

ADF50109;

ADP50109/c ID ADP5(XX AC ADP5(XX

RESULT 14

Query Match

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The invention relates to a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene comparish one or more chemical modifications and each strand of the double-stranded siNA comprises about 21 nucleotides. The siNA of the invention demonstrates antiarteriosclerotic, neuroprotective, cot in cotropic, antiparkinsonian and anticonvulsant activities and may be useful for down-regulating the expression of an endogenous mammalian target gene and therefore in the treatment of any disease or condition target gene and therefore in the treatment of any disease or condition target gene and therefore in the treatment of any disease or condition tissue or organism. The disease or condition may include pulmonary disease such as restenois, atherosclerosis, Alzheimer's disease, Parkinson's disease, epilepsy, dementia, huntington's disease or amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for gene therapy applications. The current sequence is that of the siNA DNA-RNA bybrid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New double-stranded short interfering nucleic acid molecule, useful for dwn-regulating the expression of an endogenous mammalian target gene or for tracting diseases that respond to modulation of gene expression or activity.
Alzheimer's; Parkinson's; epilepsy; dementia; huntington's; amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chowrira B, Pavco P, Fosnaugh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 12.8; DB 10; Length 21; 56.2%; Pred. No. 1.4e+04; ive 5; Mismatches 2; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen J, Beigelman L, Chowr
Jamison S, Usman N, Thompson J;
                                                                                                                                                                                                                                                         20-FEB-2002; 2002US-0358580P.

11-MAR-2002; 2002US-0363124P.

06-JUN-2002; 2002US-0386782P.

29-AUG-2002; 2002US-0406784P.

05-SEP-2002; 2002US-0408378P.

09-SEP-2002; 2002US-040929P.

15-JAN-2003; 2003US-0440129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SIRN-) SIRNA THERAPEUTICS INC
                                                                                                                                                                                                                     20-FEB-2003; 2003WO-US005028
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                                                                                                                              WO2003074654-A2.
                                                               Unidentified
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                                                                                          Synthetic.
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Search completed: June 9, 2006, 00:12:32 Job time: 290 secs |::|:|||||| :|:| 4 GUCUCUGAAGACUCUG 19 셤

6 GTATCTGAAGAGTCTG 21 9; Conservative

Local Similarity

Matches Best

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8, 2006, 21:45:36 ; Search time 290 Seconds (without alignments) 528.929 Million cell updates/sec
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SUMMARIES	ΙD	AAZ50444	AAX96007	AAI 98006	ACA92364	ADG33930	ADJ66835	ADR72987	AEB18062	AAF85459	AEC52046	AEC51906	AEC51766	AAA60336	AAS99071	AAT33010	ABK87666	ADA66516	ADG89282
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Best Local Similarity

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library and has homology to the EST AAR00504. PB39 gene is located on chromosome lipli.1-11.2. Abnormally high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of differing aggressiveness and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34584-AAX35879) can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
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Pred. No. 0.6;
Mismatches 0; Indels
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                                                                                                                                                                                                         Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 1792; Disclosure; 1912pp; English
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69.1%; Score 15.2; DB 2; Length 20;

Query Match

Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PonA, Hypc, Lyas, YefW, ABCI or Omploo protein of Lawsonia intracellularis. The sequences can be used in vaccines for the prevention of Lawsonia intracellularis infection. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                   HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
                                                                                                                                                                                                                       Lawsonia intracellularis protein related oligonucleotide SEQ ID NO: 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; 88; antibacterial; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; Lawsonia intracellularis infection; Orf1; pig; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides isolated polynucleotides encoding HtrA
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawsonia intracellularis polynucleotide and encoded protein, used to prevent Lawsonia intracellularis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 21;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
Pred. No. 1.4e+03;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 13.2; DB 4; Best Local Similarity 83.3%; Pred. No. 1.4e+04; Matches 15; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawsonia intracellularis DNA PCR primer #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 55; 67pp; Japanese.
                                         20
            0;
                                                                   20 GCCTGTTCCAGATAGAAAG 1
                                                                                                                                                                                                                                                              vaccine; PCR primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 regracadeaaaade 19
                                         1 GCATGTTACAGGTAGAAAG
                                                                                                                                       AAI98006 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000; 2000JP-00320736.
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0160922P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TGTTACAGGTAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA92364 standard; DNA; 21
                                                                                                                                                                                           20-NOV-2001 (first entry)
            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                         Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-592540/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003021802-A1
                                                                                                                                                                                                                                                                                                                    JP2001169787-A.
                                                                                                                                                                                                                                                                                                                                                                                                  22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                  AAI98006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA92364;
              Matches
                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                         AA198006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA92364
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Example 2; SEQ ID NO 50; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР.
                22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160922P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000; 2000US-00689065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ66835 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER INC.
(PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-895290/82.
                                                                                                                                                            WPI; 2003-900619/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                       (ROSE/) ROSEY B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6605696-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ66835;
                                                                                                                          Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
ADJ66835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding Lawsonia intracellularis Htrh, Ponh, Hypc, Lyss, Ycfw, ABC1 or Omp100 protein. The invention also relates to a genetic construct comprising a polynucleotide molecule that can be used to alter a Lawsonia gene, comprising a polynucleotide molecule comprising a sequence that is otherwise the same as ancleotide sequence of a htrh, ponh, hypc, lyss, otherwise the same as ancleotide sequence of a htrh, ponh, hypc, lyss, otherwise the same as ancleotide sequence of a htrh, ponh, hypc, lyss, otherwise to comprising a sequence that naturally flanks in mutations capable of altering the above mentioned genes or a polynucleotide molecule comprising a sequence that naturally flanks in situ the ORF of the htrh, ponh, hypc, lyss, ycfw, abcl or omp100 gene or its homologue. The invention also relates to a fusion protein of a polypeptide comprising an epitope of Htrh, Ponh, Hypc, Lyss, Ycfw, ABC1 or derivative. The invention further relates to a substantially pure composite of the invention and compositions of the present invention are useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. Sequences ACA92124-ACA92415

proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide molecule comprising a
                                                                                                                                                                                                                                                              New isolated Lawsonia intracellularis polymucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawsonia intracellularis; HtrA; PonA; HypC; LysS; YcfW; ABC1; Ompl00; pig; 88; sequencing; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 9; Length 21;
Pred. No. 1.4e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

    L. intracellularis sequencing primer #26.

                                                                                                                                                                                                                                                                                                                                     Example 2; Page 46; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TGTTACAGGTAGAAAGC 21
                                                                               22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
                                              01-AUG-2002; 2002US-00210296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2003; 2003US-00449462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.0%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG33930 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawsonia intracellularis,
                                                                                                                                                                                                                             WPI; 2003-416977/39
                                                                                                                                                      (ROSE/) ROSEY E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003202983-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2004
             30-JAN-2003
                                                                                                                                                                                           Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG33930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
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The invention relates to a new isolated polynucleotide molecule which encodes Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein. The methods and compositions of the present invention are useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; vaccine; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; diagnostic agent; infection; pig; porcine proliferative enteropathy; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Lawsonia intracellularis polypeptides, useful as vaccines, as diagnostic agents, or in preventing infections in susceptible animals such as pigs, e.g. porcine proliferative enteropathy.
New isolated Lawsonia intracellularis polynucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 13.2; DB 10; Length 21; 83.3%; Pred. No. 1.4e+04; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawsonia intracellularis PCR primer SegID50.
                                                                                                                                                                                    Example 2; SEQ ID NO 50; 66pp; English.
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AEB18062 standard; DNA; 21 BP.

(first entry)

08-SEP-2005

AEB18062;

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This invention relates to a novel isolated polypeptide derived from Lawsonia intracellularis. The invention may be useful for the development of compounds with an antibacterial activity or a vaccine. Specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; infection; primer; probe; ss.
                                                      claimed are L intracellularis proteins, such as HtrA, PonA, HypC, LysS, YcfW, ABC1 and Omp100 proteins. The invention may be useful for the development of vaccines, diagnostic agents, or in preventing L intracellularis infections in susceptible animals such as pigs, for example porcine proliferative enteropathy. The present sequence is that of a PCR primer which was used for amplification and/or sequencing of a region of L intracellularis DNA during the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polynucleotide comprising Lawsonia intracellularis nucleotide sequence that encodes HtrA, PonA, HypC, LysS, YcfW, ABC1 or Ompl00 protein or its essential portion, useful as diagnostic agent.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of the
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                 60.0%; Score 13.2; DB 10; Length 21; 83.3%; Pred. No. 1.4e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                          Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawsonia intracellularis DNA sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 50; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                               regracaccaacaaaacc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999; 99US-0160922P.
20-OCT-2000; 2000JP-00320736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2004; 2004JP-00092095
                                                                                                                                                                                                                                                                                   ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                          4 TGTTACAGGTAGAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR72987 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-597336/58
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2004229667-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2004.
                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR72987;
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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The invention relates to Lawsonia intracellularis Hypc protein and a nucleotide sequence that encodes L. intracellularis HtrA, PonA, Hypc, Lyss, YcfW, ABCI, orfl and Omp100 protein. The invention also relates to an immunogenic composition or vaccine comprising an immunogenic amount of the proteins of the invention in combination with a pharmaceutical carrier. The composition is useful for diagnosing or preventing infections caused by L. intracellularis porcine proliferative enteropathy (PPE) in susceptible animals such as pigs. The present sequence is a primer used for sequencing pRR392 Lawsonia intracellularis gene cluster B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Lawsonia intracellularis HypC proteins useful for diagnosing or preventing infections caused by L. intracellularis in susceptible animals, such as pigs.
                                                                                                                           Diagnosis; vaccine; infection; antimicrobial; enteropathy;
gastrointestinal-gen.; gastrointestinal disease; HtrA; PonA; HypC; Orfl;
primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Motilin receptor; gastrointestinal disease; gastric motility disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide in unique region in exon 1 of rabbit motilin receptor.
                                                                                                 SEO:
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 13.2; DB 14; Length 21; 83.3%; Pred. No. 1.4e+04; tive 0; Mismatches 3; Indele (
                                                                                               L. intracellularis gene cluster B sequencing primer, ER178,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing HtrA, PonA, HypC and Orfl genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 50; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 rigeracageaagaaage 19
                                                                                                                                                                                                                                                                                                                         22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
                                                                                                                                                                                                                                                                                         30-MAY-2003; 2003US-00449648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TGTTACAGGTAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF85459 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-2001 (first entry)
                                                                                                                                                                                             Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-457804/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       (ROSE/) ROSEY E
                                                                                                                                                                                                                         US2005143561-A1.
                                                                                                                                                                                                                                                           30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                        Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF85459;
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Gaps

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Score 13.2; DB 13; Length 21; Pred. No. 1.4e+04;); Mismatches 3; Indels (

;

15; Conservative

Matches

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Local Similarity

Query Match

83.3%;

60.0%;

4 TGTTACAGGTAGAAAGC 21 recracaccaacaaacc 19

WO200132710-A1.

10-MAY-2001

29-OCT-1999;

Tan C,

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The invention relates to an antisense oligonucleotide or its active derivative selected from AEC46374-AEC46395, targeting human interleukin-CC derivative selected from AEC46374-AEC46395, targeting human interleukin-CC derivative selected from AEC46374-AEC46395, targeting human interleukin-CC oligonucleotide (or its active derivative, by adding consecutive oligonucleotide chain), a pharmaceutical composition comprising to nucleosides and linker stepwise or by cutting the Oligonucleotide out of composition for treating cancer. The oligonucleotide is an antisense composition for treating cancer. The oligonucleotide is an antisense coligonucleotide inhibiting the synthesis of proteins involved in the formation of metastases. The oligonucleotide is an antisense coligonucleotide inhibiting the production of transforming growth factor (TGP)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules coligonucleotide inhibiting the production of transforming growth factor (TGP)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules colimbiated in the preparation of a pharmaceutical composition for inhibiting the production of a pharmaceutical composition for inhibiting the production of a pharmaceutical composition for inhibiting the preparation of a pharmaceutical composition for inhibiting the production of a pharmaceutical composition for inhibiting the cancer, bronchogenic carcinoma, carcinoma, colorectal carcinoma, carcinoma, colorectal carcinoma, carcinoma, lung carcinoma, medullary carcinoma, and and neck cancer, paptilary carcinoma, medullary carcinoma, paptilary adenocarcinoma, prostate cancer, small concer, paptilary carcinoma, negatical cancer, paptilary carcinoma, paptilary adenocarcinoma, prostate cancer, small cancer, squamous cell carcinoma, carcinoma, sectal cancer, squamous call carcinoma, carcinoma, sectal cancer, squamous call carcinoma, tertinoma, tertinoma, uterine cancer, squamous cancer, squamous call carcinoma, tertinoma, tertinoma, production cancer, squamous cancer, squamous call carcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma, memangioblastoma, medullablastoma, melanoma, mesorbastoma, neuroblastoma, neurofibroma, pinealoma, retinoblastoma, sarcoma, seroma, trachomas, wilm's tumor and/or myeloma, multiple. The present sequence is an
                                                                                                                                             New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
           Stauder G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor beta; TGF-beta-3; antisense therapy; antisense oligonucleotide; ss; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 87.5%; Score 12.8; DB 14; Length 18; Similarity 87.5%; Pred. No. 2.2e+04; Pred. No. 2.2e+04; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide targeting human TGF-beta-3 #304.
           Jachimczak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense oligonucleotide targeting human TGF-beta-3
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        Schlingensiepen K, Schlingensiepen R,
                                                                                                                                                                                                                                                                                      Claim 4; Page 71; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEC51906 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TACAGGTAGAAAAGCC
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                                  Bischof A, Hafner M,
                                                                                         WPI; 2005-630685/64.
                                                                                                                                                                                                                                    treating cancer.
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Local b...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEC51906;
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Matches
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        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP85456-60 represent polynucleotide sequences from the unique region of exon 1 of a rabbit motilin receptor gene. The specification describes an unique sequence present in exon 1 of the motilin receptor, which is not present in human or Sphaeroides nephelus 7587 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polynucleotides and polypeptides are useful for treating compounds which are useful for treating gastrointestinal diseases and disorders such as gastric motility disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligonucleotide targeting human TGF-beta-3 #444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 59.1%; Score 13; DB 4; Length 22;
1 Similarity 100.0%; Pred. No. 1.8e+04;
13; Conservative 0; Mismatches 0; Indels
gastroparesis; irritable bowel syndrome; diarrhoea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEC52046 standard; DNA; 18 BP.
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                                                                                                                                                                                                                      25-OCT-2000; 2000WO-US029426
                                                                                                                                                                                                                                                                                99US-0162264P
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01-APR-2004; 2004US-0558135P.
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                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC.
                                                       Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diarrhea in humans.
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Matches 13; Conserv
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Query Match

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Gapa

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WO2005084712-A2.

15-SEP-2005.

Homo sapiens

AEC52046;

Transforming growth factor beta; TGF-beta-3; antisense therapy; antisense oligonucleotide; ss; cancer; cytostatic.

Antisense oligonucleotide targeting human TGF-beta-3 #164.

17-NOV-2005 (first entry)

AEC51766;

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The invention relates to an antisense oligonucleotide or its active derivative selected from AEC46374-AEC46395, targeting human interleukin-
10 (IL-10). Also included are a process of manufacturing the antisense oligonucleotide (or its active derivative, by adding consecutive coligonucleotide chain), a pharmaceutical composition comprising the antisense oligonucleotide chain), a pharmaceutical composition comprising composition for treating cancer. The oligonucleotide is an antisense composition for treating cancer. The oligonucleotide is an antisense coligonucleotide inhibiting the synthesis of proteins involved in the formation of metastases. The oligonucleotide is an antisense coligonucleotide inhibiting the production of transforming growth factor (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules (CAMS), integrins, selectins, metalloproteases (MMPB), their tissue cinhibitors (TIMPB) and/or interleukins 10. The oligonucleotides are cinhibitors (TIMPB) and/or interleukins 10. The oligonucleotides are useful for the preparation of a pharmaceutical composition for inhibiting cancer, eg. bile duct carcinoma, bladder carcinoma, cuseful for treating cancer, bronchogenic carcinoma, carcinoma of the brain tumor, breast cancer, bronchogenic carcinoma, carcinoma, cervical cancer, ceptibelial carcinoma, carcinoma, carcinoma, carcinoma, carcinoma, carcinoma, carcinoma, lugarented carcinoma, carcinoma, lugarented cancer, espithelial carcinoma, esphageal cancer, gall bladder carcinoma, lugarented cancer, hepatocellular cancer, cancer, head and neck cancer, hepatocellular cancer, luker, herman carcinoma, medullary carcinoma, non-small cell cancer, head and neck cancer, hepatocellular cancer, and carcinoma, medullary carcinoma, non-small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma, papillary carcinoma, papillary adenocarcinoma, prostate cancer, small intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland carcinoma, sub ancer, squamous cell carcinoma, testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma, deurofibroma, pinaloma, retinoblastoma, asrcoma, seminoma, trachomas, Wilm's tumor and/or myeloma, multiple. The present sequence is an antisense oligonucleotide targeting human TGF-beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stauder G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jachimczak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlingensiepen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 70; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egger T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ANTI-) ANTISENSE PHARMA GMBH
                                                                                                                                                                                                      28-FEB-2005; 2005WO-EP002101.
                                                                                                                                                                                                                                                                                                             27-FEB-2004; 2004EP-00004478
                                                                                                                                                                                                                                                                                                                                                             01-APR-2004; 2004US-0558135P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schlingensiepen K, Sc
Bischof A, Hafner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-630685/64.
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Best Local Similarity
WO2005084712-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating cancer.
                                                                                                      15-SEP-2005
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New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for

Claim 4; Page 70; 106pp; English.

treating cancer.

Stander G;

Schlingensiepen R, Jachimczak P, 1, Egger T;

(ANTI-) ANTISENSE PHARMA GMBH

Schlingensiepen K, Sc Bischof A, Hafner M, WPI; 2005-630685/64.

28-FEB-2005; 2005WO-EP002101. 27-FEB-2004; 2004EP-00004478. 01-APR-2004; 2004US-0558135P.

WO2005084712-A2 Homo sapiens.

15-SEP-2005

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The invention relates to an antisense oligonuclectide or its active derivative selected from AEC46395, targeting human interleukin-
CC derivative selected from AEC46394-AEC46395, targeting human interleukin-
CC 10 (IL-10). Also included are a process of manufacturing the antisense oligonuclectide chain), a pharmaceutical composition comprising the nucleosides and linker stepwise or by cutting the oligonuclectide chain), a pharmaceutical composition comprising the antisense oligonuclectide chain), a pharmaceutical composition comprising the antisense oligonuclectide inhibiting the synthesis of proteins involved in the formation of metastases. The oligonuclectide is an antisense oligonuclectide inhibiting the production of transforming growth factor (TGP)-beta 1, TGP-beta 2, TGP-beta 3, cell-cell adhesion molecules oligonuclectide inhibiting the production of transforming growth factor (TGMS), integrins, selectins, metalloproteases (WMPS) their tissue inhibitors (TIMPS) and/or interleukins 10. The oligonuclectides are useful for the preparation of a pharmaceutical composition for inhibiting the formation of metastases in cancer treatment. The oligonuclectides are useful for treating cancer, bronchogenic carcinoma, carcinoma, carcinoma, colon carcinoma, colon carcinoma, colon carcinoma, colon carcinoma, colorectal carcinoma, employmential cancer, epithelial carcinoma, employmential cancer, epithelial carcinoma, espancers gastric cancer, papithelial carcinoma, colon carcinoma, olon carcinoma, olon carcinoma, olon carcinoma, olon carcinoma, olon carcinoma, olon carcinoma, colorectal carcinoma, employment, prostate cancer, sapillary adenocarcinoma, papillary adenocarcinoma, prostate cancer, sapillary carcinoma, papillary adenocarcinoma, prostate cancer, sapillary carcinoma, rectal cancer, renal calcinoma, papillary adenocarcinoma, papillary adenocarcinoma, papillary accomen, sepancer, sequence, renal cancer, sequence, carcinoma, attentine cancinoma, uterine cancer, sequence cancer, sequence cancer, sequence cancer, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma,
neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
Wilm's tumor and/or myeloma, multiple. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense oligonucleotide targeting human TGF-beta-3.
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DB 14; Length 18; Pred. No. 2.2e+04; Score 12.8; 58.2%; Best Local Similarity Query Match

AEC51766 standard; DNA; 18 BP

AEC51766/c ID AEC51 XX

RESULT 12

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Gaps

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22

17 TACAGGAGAGAATCC 2 7 TACAGGTAGAAAAGCC

1 Similarity 87.5%; 14; Conservative

Matches

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Rommens JM;

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Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell.
   gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                        Tavtigian SV, Teng DHF, Simard J,
                                                                                                                                                                                                                                                                                    Example 8; Page 74; 239pp; English.
                                                                                                                                                      (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                        07-MAY-2001; 2001WO-US014602.
                                                                                                                                05-MAY-2000; 2000US-00564805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ATGTTACAGGTAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 ATGTCACAGGCAGAAA
                                                                                                                                                                                                               WPI; 2002-066599/09
                                                           WO200185911-A2
                                      Homo sapiens.
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                                                                                  15-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human version of the gene is found on chromosome 17p. Some alleles cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a primer used in the isolation of the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                              Human; mouse; prostate cancer predisposing gene; HPC2;
human chromosome 17p; gene therapy; peptide therapy; drug design;
PCR primer; sequencing primer; ss.
                                                                                                                                                                        Human HPC2 cDNA exon 18 mutation screening primer SEQ ID NO: 157.
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  Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 61; 157pp; English.
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                                                                                                    AAA60336 standard; DNA; 19 BP
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                                            TACAGGGAGAAAATCC 3
                                                                                                                                                                                                                                                                                                                                                              (MYRI-) MYRIAD GENETICS INC.
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                     7 TACAGGTAGAAAAGCC
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14; Conservative
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     Tavtigian SV,
                                                                                                                                                                                                                                             Homo sapiens.
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic resquents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe; HMG box; human; bovine; sex; animal; birth; ss.
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ID AAT33010 standard; DNA; 20 BP.
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(KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU,

WPI; 1996-336575/34.

Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of unborn animals.

Example 2; Page 6; 21pp; Japanese.

The primers AAT33009-10 were used to amplify a fragment of the gene encoding a mouse SRY-related protein (AAT33007). This primer corresp. to bases 7156-7175 of the mouse gene. The amplified fragment was used to screen a mouse genomic library. The screen isolated 4 EcoRI fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a human SRY HMG box sequence between bases 7154-7393. Similarity with the human SRY HMG box sequence for use as a probe to isolate the bovine SRY-related gene (AAT33008). The mouse and bovine genes are useful for determining the sex of an animal prior to birth

Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Gaps ö Query Match 58.2%; Score 12.8; DB 2; Length 20; Best Local Similarity 87.5%; Pred. No. 2.2e+04; Matches 14; Conservative 0; Mismatches 2; Indels

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7 TACAGGTAGAAAGCC 22

Search completed: June 8, 2006, 21:51:02 Job time: 294 secs

20 TGCAGGTGGAAAAGCC 5 셤 ઠે

us-09-743-825-7.rng

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Searched:

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21 bp DNA linear PAT 27-AUG-2002 Lawsonia intracellularis protein and methods and materials relating thereto.
BD014939.1 GI:22555746
JP 2001169787-A/43.
      AR234243 Sequence
AR4291044 Sequence
AR47616 Sequence
AR47616 Sequence
AR271107 Sequence
AR271107 Sequence
AR271485 Sequence
AR271485 Sequence
AR17895 Sequence
AR287958 Sequence
AR405002 Sequence
AR4071329 Sequence
AR57186 Sequence
AR57186 Sequence
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AR57186 Sequence
AR57187 Sequence
AR57189 Sequence
CS102002 Sequence
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AR3496 Synthetic
AR3496 Synthetic
AR3496 Synthetic
AR162418 Sequence
AR3496 Synthetic
AR405006 Sequence
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Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polymucleotides and uses thereof
Patent: US 6559294-A 5333 06-MAY-2003;
Genset, S.A.;
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Sequence 5333 from patent US 6559294.
AR314796
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/organism="unknown"
/mol_type="genomic DNA"
       AR234243
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AR293044
AR29864
AR271160
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AR271170
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17; Conservative
Unclassified.
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AR374844
AR374844
BD2331604
AR652656
AX405008
CQ975123
CS009920
CS009920
CS060757
CS060758
AR167519
AR167519
      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
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AR37484
AR33516
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AR31469
AR631469
AR65265
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Gapop 10.0 , Gapext 1.0
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22
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2: gb_pat: *
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linear
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                       DNA
                   AX139516 21 bp
Sequence 50 from Patent EP1094070.
AX139516

    .19
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06-NOV-1998 US 60/1074
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JP 2002529065-A/156
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                                                                  Rosi,I.b.
Lawsonia intracellularis protein and methods and materials relating
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C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/53,G01N33/569// PC
              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Lawsonia.
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    /organism='Lawsonia intracellularis'

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Patent: US 6605696-A 50 12-AUG-2003;
Pfizer, Inc. and Pfizer Products, Inc.; New York, NY
Location/Qualifiers
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/organism="Lawsonia intracellularis"
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                                                                                                          Patent: JP 2001169787-A 43 26-JUN-2001;
PPIZER PRODUCTS INC
OS Lawsonia intracellularis
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Sequence 50 from patent US 6605696.
AR374844.1 GI:40077832
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26-JUN-2001
20-OCT-2000 JP 2000320736
22-OCT--1999 US 60/160922
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    .21
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PR 22-OCT-
PC C12N15/
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PC C12P11/1
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RESULT 4

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FEATURES

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COMMENT

ö 19 bp DNA linear PAT 17-JUL-2003 Chromosome 17q-linked prostate cancer susceptibility gene. BD231604 PC C12N15/09, A0110-1, TOTAL A1 C12N1/15, C12N1/19, C12N1/21, C12N5/ PC C07K14/47, C07K16/18, C07K16/44, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC C07K14/47, C12N1/19, C12N1/19, C12N1/21, C12 Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Lawsonia. C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/56, G01N33/57, G01N37/00,C12N15/00,A61K37/02,C12N5/00 Chromosome 17q-linked prostate cancer susceptibility gene FH Location/Qualifiers Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; 06-NOV-1998 US 60/107468 SEAN V TAVTIGIAN, DAVID H F TENG, JACQUES SIMARD, JOHANNA M PI Gaps Lawsonia intracellularis proteins, and related methods and materials Patent: EP 1094070-A 50 25-APR-2001; Pfizer Products Inc. (US) Hominidae; Homo.

1 (bases 1 to 19)

1 vatigian, S.V., Teng, D.H.F., Simard, J. and Rommens, J.M.

Chromosome 17q-linked prostate cancer susceptibility gene
Patent: JP 2002529065-A 156 10-SEP-2002;

MYRIAD GENETICS INC, THE HOSPITAL FOR SICK CHILDREN ; 0 /organism='Homo sapiens (human)'. Length 21; Indels /organism="Lawsonia intracellularis" /mol_type="unassigned DNA" /db_xref="taxon:29546"

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PAT 14-JUN-2002
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Gene expression markers for breast cancer prognosis
Patent: WO 2004065583-A 191 05-AUG-2004,
Genomic Health, Inc. (US); Rush University Medical Center (US)
Location/Qualifiers
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61.1%; Pred. No. 4.8e+05;
iive 5; Mismatches 2;
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                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/nofe="reverse primer"
                                                     DNA
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                                                                                                                        synthetic construct
synthetic construct
other sequences; artificial sequences.
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Sequence 80 from Patent WO2004111603.
CQ975123. GI:579999022
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Sangamo Biosciences Inc. (US)
Location/Qualifiers
                                               20 bp
Sequence 25 from Patent W00222634.
AX405008
AX405008.1 GI:21438223
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19 TSYKCGAGKYAGAAAGC 2
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Matches 11; Conserv
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                  RESULT 8
AX405008/c
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DEFINITION
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CQ876341/c
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Tavtigian,S.V., Teng,D.H.-F., Simard,J., Rommens,J.M., Cannon
Albright,L.A. and Neuhausen,S.L.
Chromosome 17P-linked prostate cancer susceptibility gene
Patent: US 6844189-A 157 18-JAN-2005;
Myriad Genetics, Inc., University of Utah Research Foundation and
Hospital for Sick Children; Salt Lake City, UT
Location/Qualifiers
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Monia, B.P. and Freier, S.M.
Antisense modulation of transforming growth factor-beta 3
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Best Local Similarity 87.5%; Pred, No. 4.8e+05;
Matches 14; Conservative 0; Mismatches 2;
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Location/Qualifiers
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Sequence 157 from patent US 6844189.
AR631469
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Patent: US 6884787-A 75 26-APR-2005;
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/organism="unknown"
/mol_type="genomic DNA"
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Matches 14; Conservative
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AR631469/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Modulation of elf4e expression
Modulation of 505028628-A 201 31-MAR-2005;
Patent: WO 205028628-A 201 31-MAR-2005;
Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
Location/Qualifiers
                                                                                              /mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target
sequence/siNA antisense region"
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 Patent: WO 2005007855-A 152 27-JAN-2005;
Sirna Therapeutics, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                             organism="synthetic construct"
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RNA interference mediated inhibition of B7-H1 gene expression using short interfering Nucleic Acid (siNA)

Patent: WO 200500785-A 66 27-JAN-2005;

Sirna Therapeutics, Inc. (US)

Location/Qualifiers
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                                                                   Baker, J.B., Miller, K.D., Shak, S., Sledge, G.W. and Soule, S.U. Gene expression markers for predicting response to chemotherapy Patent: WO 2004111603-A 80 23-DEC-2004; Genomic Health, Inc. (US)
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87.5%; Pred. No. 4.7e+05;
live 0; Mismatches 2;

    .21
    forganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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/db_xref="taxon:32630"
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                                    other seguences; artificial seguences.
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CS009834
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Modulation of eifte expression
Patent: WO 2005028628 A 230 31-MAR-2005;
Isis Pharmaceuticals, Inc. (US); Bli Lilly and Company (US)
Location/Qualifiers
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                                                                                Query Match 57.3%; Score 12.6; DB 2; Length 20; Best Local Similarity 78.9%; Pred. No. 6.1e+05; Matches 15; Conservative 0; Mismatches 4; Indels
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/organism="synthetic construct"
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synthetic construct
other sequences; artificial sequences.
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Search completed: June 8, 2006, 22:24:02 Job time : 1978 secs

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CO780477 BL009D
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ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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_		RESULT 1	rocas	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	OKGANISM			REFERENCE	AUTHORS		-	STILL	JOURNAL	COMMENT											FEATURES	108						•
													the result being printed,	re distribution.				Description	A7630M1 A86690A							27649514 1M0519209	-	AZ775273 2M0007F04	Œ			AZ828233 2M0105B09	Ľ	AZ3//9/1 1MU1321U3		
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut-ida.cog/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREUS27/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing projects. In
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.7%; Score 13.8; DB 11; Length 22; Best Local Similarity 88.2%; Pred. No. 7.8e+04; Matches 15; Conservative 0; Mismatches 2; Indels (
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/mol_type="genomic DNA"
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(bases 1 to 20)
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ઠે 셤 /db_xref="taxon:5691" /clone="359f10"

ORIGIN

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The
Nationalization of the constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated molectides were
ligated to the blunt ends in high molar excess. The
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose grin a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                            AZ452265 20 bp DNA linear GSS 04-OCT-2000 1M0252H06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0252H06 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurcognathi; Murcidea; Muridae; Murinae; Mus.

(bases 1 to 20)
Munn,D., Aoyagi,A., Barber,M., Bacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                             Gaps
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50.9%; Score 11.2; DB 14; Length 20; 81.2%; Pred. No. 1.4e+06; live 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: H column: 06
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC1M0252H06"
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                                                                                                                                        6 TTACAGGTAGAAAGC
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Fax: 801 585 7177
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ORIGIN

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pw042 (gil432114|gb|AR129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ775974 2000 20 bp DNA linear GSS 16-FEB-2001 2M0009H14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0009H14 F, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                   1 (bages 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 2.2e+06;
0; Mismatches 2; Indels
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606

Pax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Brror:
Plate: 0521 row: O column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT

    .22
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0521023"
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High quality sequence stop: 22.
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Mus musculus
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AZ775974
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22 bp DNA linear GSS 14-DEC-200
1M0521023F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0521023 F, genomic survey sequence.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires; Rodentia,
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/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
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Neodiplogasteridae; Pristionchus.
1 (bases 1 to 20)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppanB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39. Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: relf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Wancouver, Canada.
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                                     50.0%; Score 11; DB 11; Length 20; 100.0%; Pred. No. 1.7e+06;
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/mol type="genomic DNA"
/strāin="California"
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Pred. No. 2.2e+06;
0; Mismatches 2;
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Class: fosmid ends.
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AZ651001.1 GI:11786054
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Pristionchus pacificus
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Matches 11; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinae. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gilfa732114 gpl)AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent R. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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KBrS006K24F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS006K24, genomic survey
   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Musinae; Mus. 1 (2022)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jab host="E. coli strain XL10-Gold, T1-resistant, F./clone lib="Mouse 10kb plasmid UUGC2M library"
//orlone lib="Wouse 10kb plasmid UUGC2M library"
//orlone libe="Wouse 10kb plasmid UUGC2M library"
musculus CS7BL/6J (female) was obtained from the Jat
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC2M0274N14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42Irr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed inco
                                                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA
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2M0274N14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone_UUGC2M0274N14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
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48.2%; Score 10.6; DB 11; Length 20;
Best Local Similarity 76.5%; Pred. No. 2.7e+06;
Matches 13; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0009 row: H column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0009 row: H column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC2M0009H14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 20.
Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
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from the Jackson

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DEFINITION AZ990555/c

RESULT 7

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TTACAGGTAGAAAG 20
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Best Local Similarity 80.0
Matches 12; Conservative
           Fax: 801 585 7177
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                                                                                                                                                                                           source
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AUTHORS
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocryledons; core eudicocryledons;
rosids; eurosids II; Brassicales; Brassicacee; Brassica.

1 (bases I to 22)
Brassicacee; Brassica.

2 (contact: Beom-Seok Park
Brassica Genomics Team
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodum-Dong, Suwon, 441-707, Korea
Fax: 482-31-299-167
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                                                                                                                                                                                                                                                                                                                                                                                  Email: pbecm@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ649514 linear GSS 14-DEC-200
1M0519A09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0519A09 F, genomic survey sequence.
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1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="KBrS006K24" /lab_host="KBrS006K24" /lab_host="B. coli DH10B" /clone lib="KBrS, Brassica rapa Sau3AI BAC library" /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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47.3%; Score 10.4; DB 14; Length 22;
Best Local Similarity 91.7%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="pekinensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Tel: 801 585 5606
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  SOURCE
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AZ649514/c
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JOURNAL
COMMENT
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gij 473214 gip Jh22072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Berson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Riter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified genomic_DNA from M.
musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse_DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 bp mRNA linear EST 07-JUN-2 ED70407, 12 Zebrafiah WashU MPIMG EST Danio rerio cDNA clone IMAGE:3717229 5' similar to TR:023327 023327 HYPOTHETICAL 108.0 1 PROTEIN: ', mRNA sequence.
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                                          Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror:
Plate: 0519 row: A column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                    High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="UUGC1M0519A09"
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FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapto (gill #1732114 |gbl. #1732072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. Selomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
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1 (bases 1 to 20)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                  Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, Clone llb="Weetcor" Whose 10kb plasmid UUGCIM library" /note="Weetcor: PWDA2nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.5%; Score 10; DB 11; Length 19; ilarity 72.2%; Pred. No. 5.2e+06; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 10000 Std Error: (Plate: 0007 row: F column: 04 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC2M0007F04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 riccacacacacananacic 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces
                                                                                             plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 13; Conserv
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jeage memory. State. The mere and the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ775273 19 bp DNA linear GSS 16-FEB-2001 2M0007F04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0007F04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                 info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarbatenbank, Berlin, Germany (web address:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="26 somite embryos, adult livers, shield
stage embryos"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: T3 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 1 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 13; Conservative
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AZ775273/c
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from the Jackson

from M.

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Gaps

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REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

ORIGIN

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/mol_type="genomic DNA"
/strain="C57BL/6J"
                           clone="UUGC1M0391M24"
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AZ828233.1 GI:12998141
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Matches 13; Conserv
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AZ828233
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/organism="Schizosaccharomyces pombe"
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spo02889"
/sex="h minus"
/se
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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1M0391M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0391M24 F, genomic survey sequence.
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(Dases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
pombe
Unpublished (1998)
Contact: Mitsucki Morimyo
Genome Research Group
Genome Institute of Radiological Sciences
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Bmail: morimyo@nirs.go.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 45.5%; Score 10; DB 1; Length 20; 1 Similarity 72.2%; Pred. No. 5.3e+06; 13; Conservative 0; Mismatches 5; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: M column: 24
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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Matches 13; Conserva
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AZ585902
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of publy (1914) 4312114 [pgl AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0105B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0105B09 F, genomic survey sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus
/lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Niederhausern, A. and Wright, D., Weiss, R.
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 5.3e+06;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                           /close libe-Mouse 10kb plasmid UGCIM library...
/close libe-Mouse 10kb plasmid UGCIM library...
/mote="Westor: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomocleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114]gb|APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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1 (bases 1 to 21)

S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rallam,H., Longacre,S., Mahmoud,M., Mesen,E., Pedersen,T., Rellam,H., Longacre,S., Mahmoud,M., Mesen,E., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausers

In Dupublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105B09 F, genomic survey sequence.
                                                                                  lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
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xref="taxon:10090"
                            UUGC2M0105B09"
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High quality sequence stop: 21.
Location/Qualifiers
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Best Local Similarity 72.2
Matches 13; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil-#1732114 |gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                               /db_xref="taxon:10090"
                                                                                     /clone="UUGC2M0105B09"
strain="C57BL/6J"
                                                                                                                                         /sex="Male"
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ORIGIN

Gaps ö Query Match 45.5%; Score 10; DB 11; Length 21; Best Local Similarity 100.0%; Pred. No. 5.3e+06; Matches 10; Conservative 0; Mismatches 0; Indels

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Search completed: June 8, 2006, 23:01:53 Job time : 2264 secs

us-09-743-825-7.rni

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Sequence 5333, Ap Sequence 50, Appl Sequence 50, Appl Sequence 157, App
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6072, Ap
                                                                                                                                        8, 2006, 22:10:54; Search time 100 Seconds (without alignments) 411.644 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/FB_COMB.seq:*
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"GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-210-256A-50
US-09-564-80
US-09-68-90-157
US-09-906-158-75
US-08-840-316-53
US-08-471-971-53
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US-08-471-971-53
US-08-470-246-53
US-08-16-765-53
US-08-16-765-53
US-08-702-251-44
US-08-702-251-44
US-08-702-251-44
US-08-765-340-23
US-08-777-270-27
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                                                                                                                                                                                                                                                                                                                                                                                                                              1403666 seqs, 935554401 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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22
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Sequence Sequence Sequence

11.8 11.8 11.8

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Sequence 5333, Application US/09198452A

Sequence 5333, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevrature OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Prizer Products, Inc.
TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND TITLE OF INVENTION: MATERIALS
FILE REPERENCE: 3153.00187/PC110589A
CURRENT APPLICATION NUMBER: US/09/689,065B
CURRENT PILING DATE: 2000-10-12
PRIOR PILING DATE: 1999-10-22
PRIOR PILING DATE: 1999-10-22
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATCHIN NOS: 112
SOFTWARE: PATCHIN Version 3.2
SEQ ID NO 50
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    29, Appl
4544, Ap
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1534, Ap
79, Appl
4284, Ap
702, App
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Pred. No. 5e+02;
0; Mismatches 3; Indels
US-09-648-520B-29
US-08-985-162-704
US-08-985-162-704
US-08-985-162-704
US-08-985-162-705
US-08-985-162-705
US-08-98-162-705
US-09-31-772B-79
US-09-371-772B-4284
US-09-401-063-702
US-09-401-063-703
US-09-401-063-704
US-09-401-063-704
US-09-401-063-704
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US-09-401-063-704
US-09-401-063-704
US-09-401-063-704
US-09-401-083-706
US-08-981-988A-27
US-08-981-98A-27
US-08-981-98A-27
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US-09-531-000-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 69.1%;
1 Similarity 85.0%;
17; Conservative (
       Query Match
Best Local Similarity
Matches 17; Conserv
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US-09-198-452A-5333/c
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    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                 FARENTA NO. 5982314

FARENTA NO. 5982314

FARENTA INFORMATION:

APPLICANT: Pfizer Products, Inc.

TITLE OF INVENTION: LANGOINA INTRACELLULARIS PROTEINS, AND RELATED METHODS AND

TITLE OF INVENTION: MATERIALS

FILE REFERENCE: 3153.00355/PC10589B

CURRENT APPLICATION NUMBER: US/0/210,296A

CURRENT FILING DATE: 2002-08-01

PRIOR PLILING DATE: 1099-10-12

PRIOR FILING DATE: 1999-10-22

PRIOR PLILING DATE: 1999-11-05

PRIOR PLILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 110

SSOTUMARE: PATENTIN Version 3.2

LENGTH: 21
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GENERAL INFORMATION:

APPLICANT: Tartiqian, Sean V.

APPLICANT: Tartiqian, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US 60/107,468

FRIOR APPLICATION NUMBER: US 60/107,468

FRIOR APPLICATION NUMBER: 1998-11-05

FRIOR PRING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 157

LENGTH: 19
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                                                                                                             Query Match 60.0%; Score 13.2; DB 3; Length 21; Best Local Similarity 83.3%; Pred. No. 4.6e+03; Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-226A-50
; Sequence 50, Application US/10210296A
; Patent No. 6982314
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Patent No. 6333403
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-09-689-065B-50
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; ORGANISM: Lawsonia intracellularis
US-10-210-296A-50
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ORGANISM: Homo sapiens
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Sequence 75, Application US/09906158

Retent No. 6884787
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Monia
APPLICANT: Break M. Freier
ITILE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESS
TITLE PERFERENCE: RTS-0257
CURRENT APPLICATION NUMBER: US/09/906,158
CURRENT FILING DATE: 2001-07-14
NUMBER OF SEQ ID NOS: 168
ILENGTH: 20
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Mariad H.F.
TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene
CURRENT APPLICATION NUMBER: US/09/434,382
CURRENT FILING DATE: 1999-11-06
EARLIER APPLICATION NUMBER: US 60/107,468
EARLIER PILING DATE: 1999-11-06
WUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
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Query Match 58.2%; Score 12.8; DB 3; Length 19; Best Local Similarity 87.5%; Pred. No. 7.1e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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87.5%; Pred. No. 7.1e+03;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                   ; Sequence 157, Application US/09434382
; Patent No. 6844189
                                                                                           3 ATGTTACAGGTAGAAA 18
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Best Local Similarity 87.55
Matches 14; Conservative
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-434-382-157
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US-09-906-158-75/c
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US-08-471-971-53

Sequence 53, Application US/08471971

Sequence 53, Application US/08471971

Sequence 53, Application US/08471971

Sequence 53, Application US/08471971

FREMINGRAL INFORMATION:

APPLICANT: Tasarev, Sergei. A., Emerson,

APPLICANT: Suzanne U., Purcell, Robert H.

TITLE OF INVENTION: Recombinant Proteins Of

TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARGAN & FINNEGAN

STREET: 345 PARK AVENUE

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,971
FILING DATE: 06-UN-1995
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
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Best Local Similarity
Matches 14; Conserva
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Batent No. 6207416

GENERAL INFORMATION:
APPLICANT: Tearev, Sergei. A., Emerson,
TITLE OF INVENTION: Recombinant Proceins Of,
TITLE OF INVENTION: A Parkistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: A Parkistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: ASS PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                      Sequence 53, Application US/08840316
Patent No. 6054567
GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                           ADDRESSE; MORGAN & FININGSON.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY DISK
COMPUTER: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,316
FILING DATE: 1-APE-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
FILING DATE: 1-APE-1997
CLASSIFICATION: 424
ATTORE READATION: 424
ATTORE RECOMMUTATION: 424
ATTORE RECOMMUTATION: 424
ATTOREY AGENT INFORMATION:
MAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
TELECOMMUTATION INFORMATION:
TELECHONE: (212) 758-4800
TELECOMMUTATION INFORMATION:
TELEFRAX: (212) 758-4800
TELEFRAX: (212) 758-4800
TELEFRAX: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
ENGURNE GHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GTTACAGCCAGAAACC 18
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
US-08-840-316-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-840-316-53
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US-08-809-523-53
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPES: FLOPEY DISK
COMPUTER: 18M PC COMPATIBLE
COMPUTER: 18M PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1994
FILING DATE: 03-OCT-1994
FILING DATE: 03-OCT-1994
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: RICHARM W. BORK
REGISTRATION NUMBER: 36,459
FRIENROWED/OCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELEPRAN: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
LENGTH: 18 base pairs
TELEMEDHORE: ATTORNEY
TELEMEDHORE: ATTORNEY
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
LENGTH: 18 base pairs
TELEMEDHORE: ATTORNEY
TELEMENTER
TELEMEDHORE: ATTORNEY
TELEMEDHOR
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2 GTTACAGCCAGAAACC 18

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5 GTTACAGGTAGAAAGC 21
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Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer bind
                                          Best Local Similarity
Matches 14: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-470-246-53
                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tearev, Suzanne U., Purcell, Robert H.,
APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.
ITILE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
ITILE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
IO154
COMPUTER READBLE PORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 1.4e+04;
0; Mismatches 3; Indels
                                               APPLICATION NUMBER: USU//94,,203
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 2026-4032US2
TELECOMPUNICATION INFORMATION:
TELEFRICATION INFORMATION:
TELEFRICATION INFORMATION:
TELEFRICATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION NOMBER: US/US/VICE
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNDBER: 08/840,316
FILING DATE: 11-APR-1997
ATTORNEY/ASHT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
ESEQUENCE CHARACTERISTICS:
LENGTH: 18 DASS PAITE:
LENGTH: 18 DASS PAITE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 53, Application US/09402776
Patent No. 6458562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GTTACAGCCAGAAACC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.5%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                              US-08-471-971-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-402-776-53
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US-09-422-978-4779

Sequence 4779, Application US/09422978

Patent No. 653751

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilva

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

PILE REFERENCE: GENERAL 099-10-20

CURRENT APPLICATION NUMBER: US/09/422, 978

CURRENT PILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

MUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4779

LENGTH: 18
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                                            Gaps
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; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-09-422-978-4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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U., Purcell, Robert H.
Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
Be In Diagnostic Methods And Vaccines
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55.5%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 1.4e+04; live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.2; DB 3;
Pred. No. 1.4e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,246
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TSATEV, Sergei. A., EN APPLICANT: Suzanne U., Purcell, F TITLE OF INVENTION: Recombinant F TITLE OF INVENTION: Use In Diagno NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/08470246
Patent No. 6696242
GENERAL INFORMATION:
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14; Conservative
                                LENGTH: 18 base pairs
                                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-316-765-53
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APPLICANT: Tsarev, Sergei. A., Emerson,
APPLICANT: Stranne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES:
OORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 55.5%; Score 12.2; DB 3; Length 18; 1 Similarity 82.4%; Pred. No. 1.4e+04; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE PORM:
COMPUTER READABLE PORM:
MEDLUM TYPE: FLOPPY DISK
MEDLUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA: 08/316,765
APPLICATION NUMBER: US/08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/316,765
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: US/07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMULICATION: UNFORMATION:
TELECOMMULICATION: UNFORMATION:
TELECOMMULICATION: UNFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-0CT-1994
CLASSIFICATION 0435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 2026-4032
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SED ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
ITENTOR CHARACTERISTICS:
LENGTH: 18 base pairs
ITENTOR CHARACTERISTICS:
INFORMATION FOR SED ID NO: 53:
TERMEDISTICS: SIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/08316765
Patent No. 6706873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTACAGCCAGAAACC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-470-246-53
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US-08-316-765-53
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                                                 Gaps
                                                                                                                                                                                                                                                                                                               APPLICANT: Tsarev, Sergei. A., Emerson,
Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
A Pakkstani Strain Of Hepatitis B And Their
Use In Diagnostic Methods And Vaccines
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    Length 18;
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                                              IndelB
Score 12.2; DB 3;
Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: RICHARD W. BOTK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,475
FILING DATE: 28-NO. 6787145-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/316,765
FILING DATE: 03-OCT-1994
APPLICATION NUMBER: US/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                      US-09-724-475-53; Sequence 53, Application US/09724475; Patent No. 6787145; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        5 GTTACAGGTAGAAAAGC 21
                                                                                                                                2 GTTACAGCCAGAAACC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GTTACAGGTAGAAAGC 21
Query Match
Best Local Similarity 82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GTTACAGCCAGAAACC
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RESULT 15

PET-1089-10849A-53

FGT-1089-10849A-53

FGT-1089-10849A-53

FGT-1089-106-10849A-53

FGENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Recombinant Proteins Of

TITLE OF INVENTION: We In biagnostic Methods and Vaccines

CORRESPONDENCE: 98

CORRESPONDENCE: 98

CORRESPONDENCE: 98

COUNTRY: USA

STREET: 345 PARK AVENUE

STATE: MAW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER: BM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: BM PC COMPATIBLE

COMPUTER: NORDERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC-DS/MS-DS

FILLING DATE: 17-SEP-1992

FILLING DATE: 118-SEP-1992

ATTORNEY/AGENT INFORMATION:

FELEPHANE: (212) 758-6499

INFORMATION FOR SEQ ID NO: 53:

INFORMATION FOR SEC ID NO: 53:

INFORMATION FOR SEQ ID NO: 53:

INFORMATION: Linear

PCT-USS3-06849A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.43
Matches 14; Conservative
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Search completed: June 8, 2006, 22:48:58 Job time : 101 secs

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us-09-743-825-7.rnpbm

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Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
                                                                                                                                                                                   8, 2006, 22:49:19; Search time 857 Seconds (without alignments) 315.435 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                         US-09-743-825-7
22
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Ap.	,	29.	23.	48.	23.	48	74.	59,	75,	24.	18,	46.	13.	4	700
		333,	163654			935948	920023	935948	353174	805859	353175	117024	464518	574946	361013	29724	1250004
	Description	Sequence 5333, Ap	Sequence 163654.	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sections
SUMMARIES	αI	US-10-289-762-5333	US-10-310-914A-163654	US-10-310-914A-344929	US-11-083-784-920023	US-11-083-784-935948	US-11-101-244-920023	US-11-101-244-935948	US-10-310-914A-353174	US-10-310-914A-805859	US-10-310-914A-353175	US-10-310-914A-117024	US-10-310-914A-464518	US-10-310-914A-574946	US-10-310-914A-361013	US-11-083-784-29724	US-11-083-784-1359984
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	% Query Match	69.1	65.5	64.5	62.7	62.7	62.7	62.7	62.7	62.7	62.7	6.09	6.09	6.09	0.09	60.09	60.0
	Score	15.2	14.4	14.2	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.4	13.4	13.4	13.2	13.2	13.2
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Sequence 29724, A Sequence 135984, Sequence 225688, Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl	Sequence 248351, Sequence 566298, Sequence 221112, Sequence 157, App	Sequence 157, App Sequence 395658, Sequence 486688, Sequence 651437, Sequence 147360, Sequence 614693,	Sequence 676530, Sequence 683977, Sequence 948986, Sequence 1321930, Sequence 1517314, Sequence 1519873,	
US-11-101-244-29724 Sec US-11-101-244-1359984 Sec US-10-310-914A-225688 Sec US-10-210-296-50 Sec US-10-449-462-50 Sec US-10-449-468-50 Sec	48351 66298 21112	95658 86688 51437 7360 4693	US-11-083-784-676530 Sec US-11-083-784-683977 Sec US-11-083-784-949036 Sec US-11-083-784-949036 Sec US-11-083-784-1321930 Sec US-11-083-784-1519714 Sec US-11-083-784-1519973 Sec	
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ALIGNMENTS

US-10-289-762-5333/c

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Sequence 5333, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT GATIFEAS, R.
TITLE OF INVERVION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVERVION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVERVION: Chlamydia pneumoniae thereof, in particular for the diagnosis, prevr
TITLE OF INVERVION: And treatment of infection
FILE REPRENCE: 9710-003-999
CURRENT REPLICATION NUMBER: US/10/289,762
CURRENT PELLING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEG ID NOS: 6849
CURRENT PAPLICANTON: Bentwich Island
COURTY MATCH
SHILD FURNATION: Bentwich Island
GENERAL INPORMATION: Bentwich Island
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof CURRENT APPLICANT: Biller, WOUGH
TITLE PEPERENCE: 2003-200. CCUSO:
CURRENT PILING DATE: 2002-12-06
CURRENT PILING DATE: 2002-12-06
CURRENT PILING DATE: 2002-12-06
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US-11-083-784-935948

i Sequence 935948, Application US/11083784

i Sequence 935948, Application US/11083784

j Publication No. US2050245475A1

i GENERAL INFORMATION:

i APPLICANT: Diarmacon, Inc.

i APPLICANT: Reynolds, Ansetasia

APPLICANT: Reynolds, Ansetasia

APPLICANT: Reynolds, Ansetasia

APPLICANT: Searings, Stephen

i TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT PILING DATE: 2005-03-18

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 935948

LENGTH: 19
                                                                                          Squence 920023, Application US/11083784

Publication No. US200S0245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/110/14,333
PRIOR PLING DATE: 2003-11.14
PRIOR PLING DATE: 2003-11.14
PRIOR PLING DATE: 2003-11.14
PRIOR PLING DATE: 2003-11.14
SPRIOR FILING DATE: 2002-11.14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTHA: 19
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Pred. No. 1.6e+04;
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Best Local Similarity 88.2%;
Matches 15; Conservative
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US-11-083-784-920023
                                                        RESULT 5
US-11-083-784-920023/c
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 163654
LENGTH: 20
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Sequence 344929

Sequence 344929, Application US/10310914A

Sequence 344929, Application US/10310914A

Sequence 344929, Application US/10310914A

Sequence 344929

Sequence 344929
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8e+03;
ches 1; Indels (
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                                                                                                                                                                                              Score 14.6; DB 11; Length 22;
Pred. No. 6.5e+03;
                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                             4; Mismatches
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65.5%; Score 14.4; D
Best Local Similarity 81.2%; Pred. No. 8e+0
Matches 13; Conservative 2; Mismatches
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US-10-310-914A-163654
; Sequence 163654, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         2 CATGTTACAGGTAGAAAAGCC 22
                                                                                                                                                                                                                                                                                                                      2 CAUTUUCCAGGUGGAAAAACC 22
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Best Local Similarity 61.9%;
Matches 13; Conservative
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1053240
LENGTH: 22
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Best Local Similarity 73.7
Matches 14; Conservative
                                                                                             ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053240
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ORGANISM: Human
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Gaps

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Indels

Length 19;

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Indels

Length 19;

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Sequence 353174, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwinton:
ITILE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 353174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subjection No. US2006000332A1

Fublication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
IENGTH: 21
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
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88.2%; Pred. No. 1.6e+04;
vative 0; Mismatches 2;
1 | |::||| |:|||||
1 CAAGUUACAUGUAGAAA 17
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                             US-10-310-914A-353174
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US-10-310-914A-353174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
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                                                                                                                                                     Sequence 92023, Application US/11101244

Publication No. US2005046794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Punctional and Hyperfunctional
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Scaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional giRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 920023
LENGTHA: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 935948, Application US/11101244

| Sequence 935948, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Characon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Responds, Angela
| APPLICANT: Marball, William
| FILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: 60/502,050
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR PILING DATE: 2003-01-10
| PRIOR PILING DATE: 2003-11-14
| NUMBER OF SEQ ID NOS: 1591911
| SEQ ID NO 935948
| LENGTH: 19
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88.2%; Pred. No. 1.6e+04;
tive 0; Mismatches 2;
                       1 CAAGUUACAUGUAGAAA 17
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Matches 15, Conservative
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Best Local Similarity 70.63
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-11-101-244-920023
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ORGANISM: Homo sapiens
                                                                                                                                          US-11-101-244-920023/c
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US-10-914A-574946/c
Sequence 574946, Application US/10310914A
Sequence 574946, Application US/10310914A
Sequence 574946, Application US/10310914A
Publication No. US20060003322A1
Sequence 574946, Application US/10310914A
Publicant: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Parentin version 3.3
SEQ ID NO 574946
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US-10-914A-361013/c

Sequence 361013, Application US/10310914A

Publication No. US20060003322A1

Publication No. US2006000332A1

Publication No. US2006000332A1

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Kovzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUSOI

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 361013
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93.3%; Pred. No. 2.5e+04;
tive 0; Mismatches 1;
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Pred. No. 3.1e+04;
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Job time : 858 secs
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Human
US-10-310-914A-574946
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US-10-310-914A-361013
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Publication No. US20060003322A1
Publication No. US20060003322A1
Sublication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PLILNG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 117024
LENGTH: 19
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Publication No US20060003322A1
GENERAL INFORMATION:
A PEPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION WUBBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 46518
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                                                                                                                                                                                                                                                                                                                                       3 UGUUACAGGAAGAAG 19
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CURRENT FILING DATE: 2002-12-(NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 353175 LENGTH: 22
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Best Local Similarity 70.6'
Matches 12, Conservative
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Best Local Similarity 86.7.
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US-10-310-914A-353175
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US-10-310-914A-117024
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ORGANISM: Human
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                                                                                                                          TYPE: RNA
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November 2005

Published_Applications Mucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly publications will appear in the Published Applications Mew databases. Older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions arms of results, with the extensions of results, with the extensions Searches run against Amino Acid Published Applications produce two sets of results, with the extensions of results, with the extensions.

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Sequence 5192, Apple Sequence 5101, Apple Sequence 5279, Apple Sequence 5279, Apple Sequence 5086, Apple Sequence 5, Appli Sequence 60, Appli
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12, Appl
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Sequence 30, Appl
                                                             June 8, 2006, 22:49:54; Search time 23 Seconds (without alignments) 121.405 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                  Published Applications NA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-5192
US-11-293-697-5274
US-11-293-697-5279
US-11-293-697-5086
US-11-255-980-60
US-11-255-980-60
US-11-251-465-425
US-11-251-465-425
US-11-251-465-426
US-11-291-697-5086
US-11-251-465-426
US-11-291-697-9883-38
US-11-291-697-9883-38
US-11-293-697-5297
US-11-264-173-11
US-11-264-173-11
                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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US-11-200-624-35
US-10-511-455-77
                                                                                                                                                                                           253354 seqs, 63461778 residues
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Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
                                                                                                                                   1 gcatgttacaggtagaaaagcc 22
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Perfect score:
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APPLICANT: Lee, Nancy M
TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
FILE REFERENCE: NLEE-01001US1 MCP/MLB
CURRENT APPLICATION NUMBER: US/11/242,111
CURRENT FILING DATE: 2005-09-29
PRIOR PILING DATE: 2004-09-30
PRIOR PILING DATE: 2004-09-30
PRIOR PILING DATE: 2005-02-08
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1111, App
1143, App
98, App
1122, App
1122, App
1123, App
119, App
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US-10-511-832-90
US-11-078-073-406
US-11-078-073-406
US-11-078-073-407
US-10-511-937-868
US-10-514-776-62
US-11-158-209-920
US-11-252-276-111
US-11-252-276-111
US-10-559-415-1139-168
US-10-659-938A-122
US-10-659-938A-122
US-11-265-052-19
US-11-265-05-19
US-11-265-05-19
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US-11-265-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 36, Application US/11242111; Publication No. US20060088862A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 64
SOFWARE: Patentin version 3.3
SEQ ID NO 3.4
LENCTH: 21
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     ; ORGANISM: HUMAN
US-11-242-111-36
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APPLICANT: WELKI, Judith
APPLICANT: WINNICH, Arnold
TITLE OP INVENTION: Spinal Muscular Atrophy Diagnostic Methods
FILE REPERENCE: 2121-0140P
CURRENT APPLICATION NUMBER: US/11/222,810
CURRENT PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1995-10-19
NUMBER OF SEQ ID NOS: 65

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; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized pr
US-11-293-697-5279
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                                                                                                                                                                                                Gaps
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                                                                                                                                                 Score 10.8; DB 6; Length 21;
Pred. No. 3.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.2%; Score 10.6; DB 7; Length 20; 76.5%; Pred. No. 4.9e+03; tive 0; Mismatches 4; Indels
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Pred. No. 6e+03;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/11189279
Publication No. US20060115829A1
GENERAL INFORMATION:
APPLICANT: MAO, LI
APPLICANT: WANG, JIE
APPLICANT: WANG, JIE
APPLICANT: WANG
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: UTXC:875US
CURRENT APPLICATION NUMBER: US/11/189,279
CURRENT PRILING DATE: 2005-07-26
PRIOR PELING DATE: 2005-07-26
PRIOR PILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 44
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5279, Application US/11293697
Publication No. US20060105376A1
GENERAL INPORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT PILING DATE: 2005-12-05
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5279
LENGTH: 18
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91.7%;
                                                                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
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                                                                                                                                                                                                                                        8 ACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                   20 ACAGGTAAGAAGC 7
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Best Local Similarity 76.5
Matches 13; Conservative
                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-10-511-937-1101
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Best Local Similarity
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           SEQ ID NO 1101
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US-11-189-279-44
                                   LENGTH: 21
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND WOWER: US/10/511,937
CURRENT PILING DATE: 2004-10-19
FRIOR APPLICATION NUMBER: US/10/131,831
FRIOR APPLICATION NUMBER: US 10/131,831
FRIOR APPLICATION NUMBER: US 10/325,899
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                                                                                                                                                                                                            Indels
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                                                                                                                                                             50.0%; Score 11; DB 7; Le
100.0%; Pred. No. 3.2e+03;
tive 0; Mismatches 0;
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Pred. No. 3.8e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5192, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
    APPLICANT: HELLX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; TITLE OF INVENTION NUMBER: US/11/293,697
CURRE: FILING DATE: 2005-12-05
; PRIOR A.PLICATION NUMBER: US/10/108,260
; PRIOR PLING DATE: 2002-03-28
; NUMBER: OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5192
LENGTH: 18
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Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Seguence
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Best Local Similarity 85.7*
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-11-222-810-30
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                       SEQ ID NO 30
LENGTH: 22
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APPLICANT: HSIANG, York
APPLICANT: HSIANG, York
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Dalis G.
TITLE OF INVENTION: SELECTIVE TREATMENT OF ENDOTHELIAL SOMATOSTATIN RECEPTORS
FILE REPERENCE: 249622001101
CURRENT APPLICATION NUMBER: US 11/189,597
CURRENT FILING DATE: 2005-07-26
PRIOR PELICATION NUMBER: DCT/CA99/008800
PRIOR PLING DATE: 1999-09-01
PRIOR PLING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 12
SOFFWARE: Patentin Ver. 2.0
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APPLICANT: SWALSKY, PATRICIA
TITLE OF INVENTION: ENHANCED AMPLIFIABILITY OF MINUTE FIXATIVE-TREATED
TITLE OF INVENTION: TISSUE SAMPLES, MINUTE STAINED CYTOLOGY SAMPLES, AND
TITLE OF INVENTION: OTHER MINUTE SOURCES OF DNA
TITLE OF INVENTION: OTHER MINUTE SOURCES OF DNA
TITLE TELE REFERENCE: 47030.0014-01US
CURRENT APPLICATION NUMBER: 0211/255,980
CURRENT FILING DATE: 2005-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/679, 969
PRIOR FILING DATE: 2005-05-12
PRIOR FILING DATE: 2005-05-12
PRIOR PLING DATE: 2005-05-12
PRIOR PLING DATE: 2005-01-19
PRIOR APPLICATION NUMBER: 60/644, 568
PRIOR PRING DATE: 2005-01-19
PRIOR PRING DATE: 2005-01-29
PRIOR PLING DATE: 2004-11-29
PRIOR PLING DATE: 2004-11-29
PRIOR PLING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN NUMBER: 60/620, 926
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PEATURE:
; OTHER INFORMATION: Human SSTR3 primer
US-11-189-597-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 60, Application US/11255980
; Publication No. US20060115844A1
; GENERAL INFORMATION:
                                                     US-11-189-597-5/c
; Sequence 5, Application US/11189597
; Publication No. US20060089299A1
; GENERAL INFORMATION:
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LENGTH: 20
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1 Similarity 84.6%; Pred. No. 1.2e+04; 
11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.5%; Score 10; DB 7; Length 22; Best Local Similarity 72.2%; Pred. No. 9.9e+03; Matches 13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                 US-11-264-558-29/C

US-11-264-558-29/C

Sequence 29, Application US/11264558

Publication No. US2006008913A1

GENERAL INFORMATION:
APPLICANT: Balonomics Limited
APPLICANT: Mallace, Robyn H
APPLICANT: Mallacy, John C
APPLICANT: Mallacy, John C
APPLICANT: Harkin, Louise A
APPLICANT: Harkin, Louise A
APPLICANT: Berkovic, Samuel F
APPLICANT: Bishopens, Leanne M
TITLE OF INVENTION: MUTATION ASSOCIATED WITH EPILEPSY
FILE REFERENCE: 1386/10/2
CURRENT FILING DATE: 2005-11-01
RRIOR FILING DATE: 2002-12-20
RIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 29
LENGTH: 22
LENGTH: 22
LENGTH: 22
  1; Indels
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Sequence 5086, Application US/11293697

Sequence 5086, Application US/11293697

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA
FILE REPERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR PELING DATE: 2005-13-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5086
  Mismatches
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ORGANISM: Artificial Sequence
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11; Conservative
                                                                                                   5 CAGATAGAAAG 16
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; ORGANISM: Homo sapiens
US-11-264-558-29
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Best Local Similarity
Matches 11; Conserva
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  Matches
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GARDARAL INFORMATION:
GARDARAL INFORMATION:
GARDARAL INFORMATION:
MAPPLICANT: Vandeghinste, Nick
APPLICANT: Vandeghinste, Nick
APPLICANT: Vandeghinste, Nick
APPLICANT: Vandeghinste, Nick
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: 2001,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT PILING DATE: 2006-10-14
PRIOR FILING DATE: 2004-10-15
MUMBER OF SEQ ID NOS: 880
SOFTWARE: Patentin version 3.3
SEQ ID NO 426
LENGTH: 21
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Sequence 38, Application US/10148883

Sequence 38, Application US/10148883

Publication No. US20060115811A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins

TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins

TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins

CURRENT APPLICATION NUMBER: US/10/148,883

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US 60/171,110

PRIOR APPLICATION NUMBER: US 60/171,110

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 40

SOSTWARE: Patentin Version 3.3

SEQ ID NO 38

LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Knock-down target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5297, Application US/11293697; Publication No. US20060105376A1; GENERAL INFORMATION:
                                                                                  Sequence 426, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CATGGTCCGAGTAGAA 19
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Best Local Similarity 75.0
Matches 12; Conservative
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US-10-148-883-38
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Sequence 425, Application US/11251465

Publication No. US20060094061A1

GENERAL INFORMATION:

APPLICANT: BYPS, Reginald

APPLICANT: Tomme, Perer

APPLICANT: Tomme, Perer

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Inflammatory Diseases

CURRENT APPLICATION NUMBER: US/11/251,465

CURRENT APPLICATION NUMBER: 00/619,384

PRIOR APPLICATION NUMBER: 00/619,384

PRIOR PRIOR OF SEQ ID NOS: 880

SOFTWARE PARENTING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOFTWARE PARENTING DATE: 2004-10-15

LENGTH: 19
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Query Match

44.5%; Score 9.8; DB 7; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels
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1 Similarity 84.5%; Score 9.8; DB 6; Length 21
1 Similarity 84.6%; Pred. No. 1.2e+04;
11; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                               RESULT 11
US-10-559-415-155/C
is Sequence 155, Application US/10559415
is Publication No. US20060100132A1
GENERAL INFORMATION:
i APPLICANT: ABELIAGENEE AB et al
if TITLE OF INVENTION: Diagnostic Method
FILE REFERENCE: 101073-1P WO
CURRENT APPLICATION NUMBER: US/10/559,415
CURRENT APPLICATION NUMBER: 031081.2
FRIOR APPLICATION NUMBER: 031081.2
PRIOR FILING DATE: 2003-06-06
i NUMBER OF SEQ ID NOS: 191
i SEQ ID NO 155
i LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-10-559-415-155
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Matches 11; Conserva
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US-11-251-465-425
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TITLE OF INVENTION: Novel full length cDNA
FILE SERERENCE HANDER: US/11/293,697
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT PELLING DATE: 2005-12-05
FRIOM FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5297
TYPE: DNA
TYPE: DNA
FRICHELIS DATE: CONTRACTOR NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5297
TYPE: DNA
FROM THE SEQ ID NOS: 5408
SOFTWARE: PATENTIAL SEQUENCE
FRATURE:
CORRENTS: ACTIFICIAL SEQUENCE
FRATURE:
COTHER INPORMATION: Description of Artificial Sequence: an artificially synthesized FUS-11-293-697-5297
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42.7%; Score 9.4; DB 7; Length 18;
Best Local Similarity 90.9%; Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels
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CS018067 Sequence
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AR02390 Sequence
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BD067607 Brzymatic
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AR377036 Sequence
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AX1810829 Sequence
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CQ76685 Sequence
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BD04847 Novel pro
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Pred. No. 1.1e+05;
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Unclassified.
1 (bases 1 to 20)
Buell,G.N., Surprenant,A. and Kawashima,E.
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Buell, G.Nutter., Surprenant, A. and
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Patent: US 6133434-A 3 17-OCT-2000,
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Sequence 3 from patent US 6133434.
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100.0%; Pred
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Sequence 3 from patent US
AR275648
AR275648.1 GI:29709099
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   Unknown.
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JOURNAL
FEATURES
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AUTHORS
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AUTHORS
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BD067608 Enzymatic
AR402108 Sequence
AR027617 Sequence
DD206720 RNA Inter
DD206722 RNA Inter
DD206732 RNA Inter
DD206738 RNA Inter
DD206736 RNA Inter
DD207470 RNA Inter
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DD207473 RNA Inter
BD067609 Enzymatic
AR402109 Sequence
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671.112 Million cell updates/sec
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                                                                                                8, 2006, 23:04:25 ; Search time 2001 Seconds
            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BD067608
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Maximum DB seq length: 21
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McMatax, S., Fell, P. and McSwiggen, J. A.
Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
Patent: US 6623962-A 448 23-SRP-2003,
Sirna Therapeutics, Inc. and Aston University; Boulder, CO
Location/Qualifiers
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Unknown...
Unclassified.
1 (bases 1 to 20)
1 (bases 1 to 20)
2 (Alunter, M. George., Edwards, R. Mark., Czaplewski, L. George., and Gilbert, R. James.
Stem cell inhibiting proteins
Stem cell inhibiting proteins
Patent: US 5555301-A 134 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                           Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 bp DNA linear A17234 (SEQ ID NO: 134).
A17234.1 GI:513003
                                                                                                                                                                                                                                                                                         Query Match 61.0%; Score 12.8; DB 2; Length 1
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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    .20
    ^organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
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Patent: WO 9313206-A 134 08-JUL-1993;
Location/Qualifiers
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                                                                                                                                                                                                                      /organism="unknown"
/wol_type="genomic DNA"
     AR402108.1 GI:40149558
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                                     Unknown
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A17234/c
LOCUS
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unclassified sequences.

1 (bases 1 to .)

Akhtar, S., Fell, P. and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related
Enzymatic nucleic acid treatment of veceptors

Patent: JP 2015;11003-A 448 07-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV

PN JP 20015;11003-A/448

PD 07-AUG-2001
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Enzymatic nucleic acid treatment of diseases or conditions
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 Methods of screening modulators of mammalian P2X7 purinergic
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PN JP 201511003-A/448
PD 07-AUG-2001
PP 10-13M-1999 JP 1998512913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC C Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases o
                                                                                                                                                                                    Query Match 61.9%; Score 13; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 13; Conservative 0; Mismatches 0; Indels
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related to
levels of epidermal growth factor receptors
Location/Qualifiers
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Sequence 448 from patent US 6623962.
AR402108
               receptors
Patent: US 6509163-A 3 21-JAN-2003;
Glaxo Group Limited; Middlesex;

    17 /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

                                                                                                                   /organism="unknown"
/mol_type="genomic DNA"
                                                                                   Location/Qualifiers
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KEYWORDS
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ORGANISM
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AR402108/c
LOCUS
DEFINITION
ACCESSION
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BD067608/c
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Gaps

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Indels

Length 21;

PAT 19-JAN-2006

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Sirna Therapeutics Inc.

S Artificial Sequence

BN JP 2005517452-A/837

PD 16-JUN-2005

PP 18-FEB-2003 JP 2003569860

PR 15-JAN-2003 US 60/409293, PR

16-JUN-2002 US 60/409293, PR

11-MAR-2002 US 60/386782, PR

11-MAR-2002 US 60/386782, PR

11-MAR-2002 US 60/386782, PR

CC Description of Artificial Sequence: 81NA antisense region FH
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21 bp RNA linear PAT 19-JAN-2000 RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA).
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/note='3'-3 attached terminal deoxyabasic
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/note='5'-3 attached terminal deoxyabasic
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/note='n stands for thymidine' FT
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/note='n stands for thymidine'
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/note='2'-deoxy-2'-fluoro'
(5) . . (9)
/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
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       Short Interfering Nucleic Acid (siNA)
Patent: JP 2005517452-A 837 16-JUN-2005;

    .21
    forganism="synthetic construct"
|mol type="unassigned RNA"
|db_xref="taxon:32630"

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JP 2005517452-A/841.
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DD206728
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other sequences.

It bases artificial sequences.

Beigelman, L. and Mcswiggen, J.

RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Nucleic Acid (sina)

Beigelman, L. and Mcswiggen, J.

RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition of Sina Interference Mcdiated Inhibition of BCL2 Gene Expression Using Short Interference Mcdiated Inhibition Using Short Interference Mcdiated Inhibition Interference Mcdiated Inhibition Interference Mcdiated Inhibition Inhibition of Artificial Sequence: sina sense region FH Key Location Of Artificial Sequence: sina sense region FH FT misc_feature (20): (21)

FT misc_feature (20): (21)

FT misc_feature (20): (21)
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DD206724.1 GT:85643089

JP 2005517452-A/837.
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BCL2 Gene Expression Using
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by the requences artificial sequences.
1 (bases 1 to 2.1)
Beigelman, L. and Mcswiggen, J.
RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
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                                                                            Length 20;
                                                                                                                Indels
                                                                      Query Match
61.0%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                            DD206720 21 bp RNA RNA Interference Mediated Inhibition of Short Interfering Nucleic Acid (siNA).

    .21
    ^organism="synthetic construct"
|mol_type="unassigned RNA"
|db_xref="taxon:32630"

/organism="unknown"
/wol_type="unassigned DNA"
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DD206724/c
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synthetic construct
other sequences, artificial sequences.

Synthetic construct
other sequences; artificial sequences.

I (bases 1 to 21)

Beigelman, L. and Mcswiggen, J.

RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA)

LA Patent: JP 2005517452-A 849 16-JUN-2005;

Sirna Therapeutics Inc
OA Artificial Sequence
NN JP 2005517452-A/849

PD 16-JUN-2005 US 60/4003569860

PR 18-FBB-2003 JP 2003569860

PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR 05-SEP-2002 US 60/308905,06-JUN-2002 US 60/308905,06-JUN-2002 US 60/308905,06-JUN-2002 US 60/308909 PD 11-MAR-2002 US 60/308908 DE 11-MAR-2002 US 60/308909 DE 11-MAR-2002 US 60/30890 DE 11-MAR-2002 US 60/30890
                                            ENA Interference Mediated Inhibition of BCL2 Gene Expression Using bb206736
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/note='3'-3 attached terminal deoxyabasic
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/note='n stands for thymidine'
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/note='2'-deoxy'

(15) . . (18)

/note='2'-deoxy-2'-fluoro'

(19) . . (19)

/note='2'-deoxy'
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro
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llarity 87.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/note='2'-deoxy'
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/note='2'-deoxy'
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JP 2005517452-A/849.
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synthetic construct
synthetic construct
synthetic construct
other sequences, artificial sequences.

1 (Dases 1 to 21)
Beigelman, L. and Mcswiggen, J.

Beigelman, L. and Mcswiggen, J.

Bridelman, L. and Mcswiggen, J.

Short Interfering Nucleic Acid (siNA)

Patent: JP 2005517422-A 845 if-JUN-2005,

Dy 2005517452-A/845

PD 16-JUN-2005
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60/358580 PI
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PR 15-JAN-2003 US 60/40129, 09-SEP-2002 US 60/4081378, 29-AUG-2002 US 60/396905, 06-JUN-2002 US 60/363124, 20-FEB-2002 US
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
                                                                                                                                                                                Query Match 61.0%; Score 12.8; DB 2; Best Local Similarity 87.5%; Pred. No. 1.4e+05; Matches 14; Conservative 0; Mismatches 2;
                                            1.21
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Location/Qualifiers
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DD206732/c
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other sequences; artificial sequences.

1 (bases 1 to 21)
Jamison, S., Posunalu, C., Beigelman, L., Chourira, B., Thompson, J.,
Asuman, N., Pavco, P. and Mcswiggen, J.
RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)
Pattent: JP 2005518803-A 259 30-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
RN JP 2005518803-A/259
PD 30-JUN-2005
PP 20-FEB-2003 JP 2003573107
PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
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                                                                                                                                                                                                               I james thompson nashimu asuman, pamela pavco, james mcswiggen CC Description of Artificial Sequence: siNA sense region FH Key Location/Qualifiers
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60/406784, PR
60/363124, PR

    (1). (1)
    /note='5'-3 attached terminal deoxyabasic

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/note='3'-3 attached terminal deoxyabasic
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60/363124, PR
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/note='2'-deoxy-2'-fluoro'
/note='n stands for thymidine' FT
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/note='2'-deoxy-2'-fluoro'
(5) . . (9)
/note='2'-deoxy-2'-fluoro'
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60/386782,11-MAR-2002 US
60/358580
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          Patent: JP 2005518803-A 256 30-JUN-2005;

    .21
    forganism="synthetic construct"
|mol_type="unassigned RNA"
|db_xref="taxon:32630"

                                         OS Artificial Sequence
PN JP 2005518803-A/256
PD 30-JUN-2005
PF 20-FEB-2003 JP 2003573107
PR 15-JAN-2003 US 60/440129,
05-SEP-2002 US 60/386782,11-M
20-FEB-2002 US 60/386580
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PF 20-FEB-2003
PR 15-JAN-2003
OS-SEP-2002 US
06-JUN-2002 US
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AUTHORS
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 21)
Jamison, S., Fosunafu, C., Beigelman, L., Chourira, B., Thompson, J.,
Asuman, N., Pavco, P. and Mcswiggen, J.
Asuman, N., Pavco, Mcdiated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)
                                                                   other sequences; artificial sequences.

1 (bases 1 to 21)
Beigelman,L. and Mcswiggen,J.
RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA)
Patent: JP 2005517452-A 853 16-JUN-2005;
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RNA linear PAT 19-JAN-2006

RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA).
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60/386782, PR
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60/358580 PI
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(20). .(21)
/note='n stands for thymidine' FT
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
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                                                                                                                                                                                                                                                                 60/440129,09-SEP-2002
                                                                                                                                                                                                                                                                             60/408378, 29-AUG-2002 US
60/396905, 06-JUN-2002 US
60/363124, 20-FEB-2002 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .21
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/note='2'-deoxy'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -deoxy,
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PN JP 2005517452-A/653
PD 16-JUN-2005
PP 18-PEB-2003 JP 2003569860
PR 15-JAN-2003 US 60/40129,
OS-SEP-2002 US 60/396905, 06-JI
11-MAR-2002 US 60/363124, 20-FI
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/note='2'-de

(16) . . (16)

/note='2'-de

(17) . . (18)

/note='2'-de
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/note='2'-de
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CC Description of Artifi
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DD207467.1 GI:85645377
JP 2005518803-A/256.
                                                                                                                                                                    Sirna Therapeutics Inc
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other sequences; artificial sequences.

CE 1 (bases artificial sequences.

S Jamison, S., Fosunafu, C., Beigelman, L., Chourira, B., Thompson, J.,
Admison, S., Fosunafu, C., Beigelman, L., Chourira, B., Thompson, J.,
Adman, N., Pavco, P. and Mcswiggen, J.

RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)

Interfering Nucleic Acid (siNA)

Interference Mediated 1.0005;
Sirna Therapeutics Inc.

Sirna Therapeutics Inc.

OS Artificial Sequence

PN JP 2005518803-A/262

PD 30-UN-2005;
PP 2005518803-A/262

PP 20-FEB-2003 JP 2003573107

PR 15-JAN-2003 US 60/440319, 09-SEP-2002 US 60/409293, PR 05-SEP-2002 US 60/408378, 29-AUG-2002 US 60/363124, PR 20-FEB-2002 US 60/358880

PI sharon jamison, cathy foeunafu, leonid beigelman, baratto PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 bp RNA linear PAT 19-JAN-2006 RNA interference Mediated Inhibition of Gene Expression Using Short DD207473
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PI james thompson,nashimu asuman,pamela pavco,james mcswiggen CC Description of Artificial Sequence: siNA antisense region FH Key
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/note='Phosphorothioate 3'-Internucleotide
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/note='n stands for thymidine' FT
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/note='n stands for thymidine'
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/note='2'-deoxy-2'-fluoro'

(16) . .(16)

/note='2'-deoxy-2'-fluoro'

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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'

    .21
    forganism="synthetic construct"
|mol type="unassigned RNA"
|db_xref="taxon:32630"

    .21
    .coganism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"

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JP 2005518803-A/262.
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AUTHORS
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61.0%; Score 12.8; DB 2; Length 21;

Query Match

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Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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CW986631 KBEH013B0
CW986631 KBEH013B0
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DX068324 KBES00810
DX068324 KBES00810
CL694050 PRT0163a
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CL623467 018055770
AJ662026 AJ662026
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AZ358656 IM0101K12
BQ595520 B012693-0
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                                                                                                                                                                                                                                                                                                                                                       AZ784664 2001 20 bp DNA linear GSS 16-FEB-2001 2M0027I10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0027I10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muroidea; Muridae; Murinae; Mus.

1 (Dases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von plasmid inserts

Unpublished (2000)
          CF325351 JMT1--03-
CN497681 C07 02547
D20709 HUMGS01685
 C00979 HUMGS000336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 30, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0027 row: I column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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          CF325351

CA497681

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AJ671616

CO778852

AZ480596

AZ680035

AZ68035

CW986631

AZ633493

DX035468

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AZ63493

DX035468

AZ6203835

CL694050

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CL694050

AM775273

CL634050

AM775273

CL6343467

AJ662026

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AJ662026
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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GSS.
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Fax: 801 585 7177
 AZ784664
VERSION
KEYWORDS
SOURCE
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CAB51013 D09B11 C1
AZ495849 1M0131N22
AZ875769 2M0190A02
CZ282704 CP55h01.r
DUB31624 KRES008M0
AZ489135 1M0139H15
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AZ36835 AZ56836
AZ5785 1M0052A01
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AJ525976 1M0465C08
AZ625776 1M0465C08
AZ625776 AZ64588
AZ625776 AZ64587
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AZ625776 AZ64698
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                                                                 June 8, 2006, 23:04:50 ; Search time 2506 Seconds (without alignments) 468.598 Million cell updates/sec
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       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                              18086
                                                                                                                                                                                        48236798 segs, 27959665780 residues
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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CA851013
AZ8755849
AZ875764
CZ282704
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                                               OM nucleic - nucleic search, using sw model
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Match Length
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5

organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J"

FEATURES

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Result

|db_xref="taxon:10090" |clone="UUGC2M0027110" |sex="Male"

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Similarity
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by respected bases and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4732114 gb) AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, RRANGE
Gaston Cremieux, 91057 Evry cedex, RRANGE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.info.iogen.fr).

Location/Qualifiers
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Arabidopsis thaliana T-DNA flanking sequence, right border, clone 631B09, genomic survey sequence.
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
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EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
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Best Local Similarity
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AJ592729/c
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VERSION
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D09B11 C11_04.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D09B11 5', mRNA sequence.
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Alkharouf, M., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Roots"
/dev stage="Seedlings"
/dev stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
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1M0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
/db_xref="taxon:3702"
/clone="631B09"
/clone_lib="karabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                 Length 15;
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                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                        Query Match 48.6%; Score 10.2; DB 14; Best Local Similarity 80.0%; Pred. No. 3.3e+06; Matches 12; Conservative 0; Mismatches 3;

    .15
/note="T-DNA flanking sequence
right border"

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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
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/clone="D09B11"
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/cultivar="Peking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Alkharouf, N.W.
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Glycine max
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VERSION KEYWORDS SOURCE ORGANISM ACCESSION

AUTHORS REFERENCE

JOURNAL

COMMENT

TITLE

FEATURES

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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli Xillo-Gold (Stratagene) cells
and selected for ampicillin resistance."
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           2M0190A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0190A02 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 19)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Eose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bute
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: A column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

    19
    organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0190A02"
                                                                                                                           AZ875769.1 GI:13086107
GSS.
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Best Local Similarity 84.6
Matches 11, Conservative
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//cloue= Note= Note: Note
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1 (Dases 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmould, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
University of Utah
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84112, USA
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84.6%; Pred. No. 5.4e+06;
tive 0; Mismatches 2; Indels
one UUGC1M0331N22 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 10000 Std Brror: 0.00 Plate: 0331 row: N column: 22 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.
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/strain="C57BL/6J"
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/clone="UUGC1M0331N22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                         AZ495849.1 GI:10671571
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Gaps

RESULT 6 CZ282704

GSS 21-FEB-2001

linear

DNA

19 bp

AZ875769

RESULT 5 AZ875769 LOCUS

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Query Match

Gaps

; 0

GSS 05-OCT-2000

Euteleostomi;

5

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AZ489135 20 bp DNA linear GSS 05-OCT-200 1M0319H1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0319H15 R, genomic survey sequence.
                                                                                                                                                           / Sub species "pakinensis"

/ Ab xref="taxon:51351"

/ Clone="KBS1080031"

/ Lab host="E. coli DH108"

/ Clone="lib="KBIS, Brassica rapa Sau3AI BAC library"

/ Note="Vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa Ssp pekinensis var. Chiifu BAC library (KBIS BAC) is available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note=""Vector: PWD42IN'; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                       1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chift"
                                                                                                                                                                                                                                                                                                                                                                                                 Score 9.8; DB 14; Length 20;
Pred. No. 5.4e+06;
0; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0319H15"
                                                    Location/Qualifiers
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ilarity 84.6%;
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       Seq primer: T7
Class: BAC ends
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AZ489135
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                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.

1 (bases 1 to 20)

Logue, M.E., Wong, S., Wolfe, K.H. and Butler, G.
A genome sequence survey shows that the pathogenic yeast Candida parapsilosis has a defective WILal allele at its mating type locus Eukaryot. Cell 4 (6), 1009-1017 (2005)
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantas, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:5480"
/clone="cp25h01"
/clone_lib="Candida parapsilosis Random Genomic Library"
                                                                                                                                                                                                                                                                                                                                                                 Contact: Logue M
Department of Biochemistry, Conway Institute of Biomolecular and
Biomodical Research
University College Dublin
University Ireland
Tel: +353 1 7166885
Fax: +353 1 2837211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DU831624 22-DEC-20
KBrS008M03F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS008M03, genomic survey
sequence.
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Band sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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                     cp25h01.r Candida parapsilosis Random Genomic Library Candida
parapsilosis genomic clone cp25h01, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Candida parapsilosis"
/mol type="genomic DNA"
/strain="CLIB214"
    DNA
20 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mary.e.logue@ucd.ie
Class: plasmid ends.
                                                                                          CZ282704.1 GI:68453906
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Candida parapsilosis
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwap42 (gql 4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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PRIO130b G06 2 - PRIO130b.BR (17) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic CL681189
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (Dassel to 17)
Stintvasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appades an Aceds database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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45.7%; Score 9.6; DB 11; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.8e+06;
Matches 12; Conservative 0; Mismatches 4; Indels
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/mol_type="genomic DNA"
/strain="California"
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Best Local Similarity 90.99
Matches 10; Conservative
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bunk was blunt end-repaired with T4 DNA polymerase and T4 polymerase and polymerase bunk was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwm92 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasming NI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ308384 29-SEP-2000 LM0011K17P Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0011K17 F, genomic survey sequence.
                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Railly, M., Rose, R., Stokes, R., Stokes, R.,
Reilly, M., Rose, R., Stokes, R.,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/clone_11b="Mouse lokb plasmid UTGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Faul: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C578L/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                         AZ308384.1 GI:10348326
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ठ 셤 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

JOURNAL

COMMENT

TITLE

DEFINITION AZ316351/c

ACCESSION

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Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                           AZ328275 20-SPP-2000 1MO052A01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0052A01 F, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Unpublished (2000)
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Pax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: A column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0052A01"
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                                       8 ATCTGAAGAGTCTG 21
                                                                                                     20 Arcrcaadaracrd 7
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AZ328275/c
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiss B. Meiss Contact: Robert B. Weiss B. Weiss Contact: Robert B. Weiss Contact: Robert B. Weiss Contact: Robert B. Weiss Rosearch Bldg., 20 S. 2030 B., SLC, UT
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                                                                                                                                                                                                                                          AZ316351 20 bp DNA linear GSS 29-SEP-200
1M0034A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034A11 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: A column: 11
Seg primer: CGTTGTAAAACGACGCCAGT
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/db_xref="taxon:10090"
/clone="UUGC1M0034A11"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                AZ316351
AZ316351.1 GI:10364090
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ATCTGAAGAGTCTG 21
                                                         4 Arcreaderdacce 17
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Matches 11; Conserv
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AJ587417/C DEFINITION

RESULT 13

ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS REFERENCE AUTHORS

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DEFINITION ACCESSION VERSION

RESULT 14 AJ684587 LOCUS

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Anderson, S. I., Finlayson, H.A. and Archibald, A. L.
Development of CDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
("Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                            Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thalians
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
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                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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/clone_llb="CSEQRAN04"
/clone_llb="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised_llbrary
constructed from pig uterus."
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Arabidopsis thaliana (thale cress)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T_DNA integration into the Arabidopais genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 1.3e+07;
ative 0; Mismatches 0;
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EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001805 G15"
                                                                                                                                                                    (bases 1 to 16)
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Balzergue, S.
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                               Sus scrofa (pig)
Sus scrofa
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Best Local Similarity
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                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
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S. Lousers + ...

S. A Lousers + ...

S. Balzergue, S.
Direct Submission

M. Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremicux, 91057 Bryr cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced flanking the insertion T-DNA
derived sequences were removed. Information to order the
corresponding untant line and a link to a databbase providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

Ilocation/Qualifiers
                                                                                                                                                                                                                                           AJS87417 10 bp DNA linear GSS 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
                                                                                                                                                                                                                                                                                                                                                 AJSB/417.1 GI:37937041
GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="275G07"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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  Indels
  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

    10
    note="T-DNA flanking sequence"

  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBŌ Rep. 3 (12), 1152-1157 (2002)
12446565
                                                                                                                                                                                                                                                                                  275G07, genomic survey sequence.
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AJ684587
AJ684587.1 GI:49417177
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                                                   4 GCGTATCTGAAGAG 17
                                                                                                        19 GCGTACCTGTAAAG 6
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  Conservative
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11;
                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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Gaps

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1. .18
/organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
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/clone="073612"
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/cocype="Wassilewskija"
/ note="T-DNA flanking sequence
left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.9%; Score 9; DB 14; Length 18; Best Local Similarity 100.0%; Pred. No. 1.3e+07; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 9, 2006, 00:19:59 Job time: 2510 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ATCTCAAGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . misc_feature
                                                                                                                                                                                                              FEATURES
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June 8, 2006, 23:38:20 ; Search time 100 Seconds (without alignments) 392.933 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                     Run on:
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1 ctggcgtatctgaagagtctg 21 US-09-743-825-8 21 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1403666 segs, 935554401 residues Searched:

538872 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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| FBNG_Calerra_SID33/ptodata/2/ina/6_COMB.seq:*
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| FBNG_Calerra_SID33/ptodata/2/ina/RE_COMB.seq:* Issued Patents NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

i		46			SUPERSTERS	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
г	13	61.9	20	<u>س</u>	US-08-842-079-3	Sequence 3. Appli
7	13	61.9	20	e	US-09-638-857-3	'n
о О	12.8	61.0	17	٣	US-08-985-162-448	44
Ω 4.	12.8	61.0	17	n	US-09-401-063-448	
r S	12.8	61.0	20	~	US-08-450-905B-134	Sequence 134, App
y U	12.8	61.0	20	٣	US-07-982-759F-134	Sequence 134. App
0	12.2	58.1	17	٣	US-08-985-162-449	Sequence 449. App
ω υ	12.2	58.1	17	ო	US-09-401-063-449	Sequence 449, App
6	12.2	58.1	20	~	US-08-717-291-8	8. An
10	12.2	58.1	20	٣	US-08-728-603-8	Sequence 8. Appli
c 11	12	57.1	20	٣	US-09-433-699-73	73
12	11.8	56.2	16	m	US-09-371-772B-5737	573
13	11.8	56.2	16	Ŋ	US-10-138-674B-5737	
14	11.8	56.2	17	~	US-07-852-260-4	-
15	11.8	56.2	17	7	US-07-936-421-18	18
16	11.8	56.2	17	ď	US-08-461-503-4	4
c 17	11.8	56.2	17	m	US-08-985-162-447	447
18	11.8	56.2	17	٣	US-08-465-250-4	4.
19	11.8	56.2	17	m	US-09-371-772B-4438	443
c 20	11.8	56.2	17	ო	US-09-401-063-447	Sequence 447, App
21	11.8	56.2	17	Ŋ	US-10-138-674B-4438	4438
22	11.8	56.2	17	Ŋ	US-10-138-674B-7389	
c 23	11.8	56.2	20	3	US-09-488-857B-38	

1366, Ap	9. App	9. App	Appl		Appl.	Appl	1916. Ap	6486, Ap	Appl		930. App	450, App	•	4879, Ap	5682, Ap	Appl .		6. App		٠.	
		12	8	276	12	12,	19	_		68			450,	48		57,	46	466	46	22	23
Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-198-452A-1366	US-09-478-189-118	US-09-280-805-129	US-09-517-467B-30	US-09-198-452A-2767	US-09-657-289A-12	US-10-130-158A-12	US-09-657-472-1916	US-09-422-978-6486	US-08-602-093-12	US-09-906-158-68	US-10-002-623-930	US-08-985-162-450	US-09-401-063-450	US-10-156-306B-4879	US-09-422-978-5682	US-08-555-678-57	US-09-422-978-4659	US-09-696-791-466	US-09-696-791-467	US-09-488-671-22	US-09-488-671-23
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20	21	20	20	50	20	20	21	19	50	20	20	11	11	17	18	19	19	19	19	20	50
56.2	56.2	55.2	55.2	55.2	55.2	55.2	55.2	54.3	54.3	54.3	54.3	53.3	53.3	53.3	53.3	53.3	53.3	53.3	53.3	53.3	53.3
11.8	11.8	11.6	11.6	11.6	11.6	11.6	11.6	11.4	11.4	11.4	11.4	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2
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24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-08-842-079-3
                                                                                                APPLICANT: BUELL, GARY N.
APPLICANT: BUELL, GARY N.
APPLICANT: SURPRENANT, ANNARIE
APPLICANT: KAMASHIMA, ERIC
TITLE OF INVENTION: A PURIBREGIC RECEPTOR
FILE REFERENCE: 1430-160
CURRENT APPLICATION NUMBER: US/08/842,079
CURRENT FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET: 2.0
SOFTWARE: PATENTIN VET: 2.0
                      Sequence 3, Application US/08842079; Patent No. 6133434; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
US-08-842-079-3
```

Gaps ö 61.9%; Score 13; DB 3; Length 20; 100.0%; Pred. No. 3.6e+03; ive 0; Mismatches 0; Indels Query Match 61.9 Best Local Similarity 100. Matches 13; Conservative

3 GGCGTATCTGAAG 15

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US-09-638-857-3 g

Sequence 3, Application US/09638857;
Saguence 3, Application US/09638857;
Satent No. 6509163;
GENERAL INPORMATION:
APPLICANT: BUELL, GARY N.
APPLICANT: SURRENANT, ANNWARIE
APPLICANT: KARASHIMA, ERLC
TITLE OF INVENTION: A PURINERGIC RECEPTOR;
FILE REFERENCE: 1430-160;
CURRENT APPLICATION NUMBER: US/09/638,857;
CURRENT FILING DATE: 2000-08-15;
PRIOR APPLICATION NUMBER: 08/42,079
PRIOR PILING DATE: 1997-04-28;
NUMBER OF SEQ ID NOS: 20

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Matches
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                                                                                                                                                                   FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-638-857-3
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Patent No. 6057156

Jeatent No. 605716

Jeatent No. 60776710

Jeatent No. 607767710

Jeatent No. 6077710

Jeatent No. 607710

Jeatent No. 607710

Jeatent No. 607710

Jeatent No. 607710

Jeatent
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                                                                                                                                                                                                                                                                                                          Query Match 61.9%; Score 13; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3.6e+03; Matches 13; Conservative 0; Mismatches 0; Indels
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 448:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.55
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGCGTATCTGAAG 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGCGTATCTGAAG 13
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                        SEQ ID NO 3
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6 GTATCTGAAGAGTCTG 21

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Gaps
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                                                                                                               Sequence 448, Application US/09401063

Sequence 448, Application US/09401063

GENERAL INFORMATION:

APPLICANT: Pall, Patricia
APPLICANT: Fall, Patricia
APPLICANT: Fall, Patricia
APPLICANT: Foll, Patricia
APPLICANT: Foll, Patricia
TITLE OF INVENTION: ENZWAMATIC NUCLEIC ACID TREATMENT:
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stem Cell Inhibiting Proteins 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
FELECOMMUNICATION INCREMENTION:
FELECOMMUNICATION INCREMENTION:
FELECOMMUNICATION INCREMENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-450-905B-134/C
Sequence 134, Application US/08450905B
Patent No. 5856301
GENERAL INFORMATION:
PAPLICANT:
TITLE OF INVENTION: Stem Cell Inhibit
NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FSELSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GTATCTGAAGAGTCTG 21
16 GTATCGAAAGAGTCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCGAAAGAGTCTG 1
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                  US-09-401-063-448/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-401-063-448
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Length 20;
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Patent No. 6057156

GENERAL INPORMATION:

APPLICANT: Pell, Patricia

APPLICANT: Pell, Patricia

APPLICANT: MCSWiggen, James

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT

TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED

TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

TITLE OF INVENTION: PACTOR RECEPTORS

TITLE OF INVENTION: PACTOR RECEPTORS

TITLE OF ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSER: LYON & LYON

ADDRESSER: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-MAR-1993
FRIOR APPLICATION NUMBER: GB 9127319.3
FRIOR APPLICATION NUMBER: GB 9127319.3
FILING DATE: 23-DEC-1991
FRIOR APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/POCKET NUMBER: 102378.120
TELECOMMUNICATION INFORMATION:
TELECHOME: 617-526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1..20
; OTHER INFORMATION: /product= "BB9513 oligomer"
US-07-982-759F-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%; Score 12.8; DB 3;
87.5%; Pred. No. 4.5e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FREESE for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
FILING TARESITION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 134: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDENBES: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTGGCGTATCTGAAGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: 1..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 CTGACGCATCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-985-162-449/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 12.8; DB 2; Length 20; 87.5%; Pred. No. 4.5e+03; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                 OURERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,905B
FILING DATE: 26-MAR-1995
PRIOR APPLICATION NUMBER: 07/982,759
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102.378.120DV-2
TELEPHONE: 617-526-6110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-500
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CRAIG, Stewart
APPLICANT: CRAIG, Stewart
APPLICANT: GEORGE, Michael
APPLICANT: EDWARDS, Richard Mark
APPLICANT: CZAPLEWSKI, iloyd George
APPLICANT: GILBERT, Richard
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..20
OTHER INFORMATION: /product= "BB9513 oligomer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-982-759F-134/c
; Sequence 134, Application US/07982759F
; Patent No. 6057123
; GENERAL INFORMATION:
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HALE and DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGGCGTATCTGAAGA 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.59
"...hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 CTGACGCATCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-450-905B-134
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Gape

Gaps

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58.1%; Score 12.2; DB 3; Length 17; 82.4%; Pred. No. 8.9e+03; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08717291; Patent No. 5908773; GENERAL INFORMATION:
                                                                                                                                                                                                                         4 GCGTATCTGAAGAGTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 CGTATCTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                        17 GGGTATCGAAAGAGTCT 1
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                                                                                                                      Query Match
Best Local Similarity 82.4°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 82.4 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
         TYPE: nucleic acid
                                                      linear
                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 14603
                                                      ; TOPOLOGY:
US-09-401-063-449
                                                                                                                                                                                                                                                                                                                                                                 US-08-717-291-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-717-291-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 449, Application US/09401063
| Patent No. 6623962|
| GENERAL INFORMATION:
| APPLICANT: Action Sequence APPLICANT: Fell, Patricia APPLICANT: McSwiggen, James APPLICANT: MCSWIGHTON: ENZYMATION: OF DISEASES OR CONDITIONS RELATED TITLE OF INVENTION: PACTOR RECEPTORS NUMBER OF SEQUENCES: 1877
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon STREET: 633 West Pifth Street STREET: 631 te 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORME
COMPUTER: ENGRAGE
COMPUTER: COMPUTER: DOS 5.0
SOFTWARE: FRACESCO for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/401,063
FILING DATE: 04 December 1997
APPLICATION NUMBER: 08/885,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY AGENT INFORMATION:
                                     NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 230/107

TELECOMMUNICATION INFORMATION:
TELEFONE: (213) 955-0440

TELEFAX: (213) 955-0440

TELEFAX: (213) 955-0440

TELEFAX: (213) 955-0440

TELEFAX: (213) 955-046

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

US-08-985-162-449
FILING DATE: 31 January 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE DOCKET NUMBER: 27 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GCGTATCTGAAGAGTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 GGCTATCGAAAGACTCT 1
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.44
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-401-063-449/c
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APPLICANT: Cesarman, Ethel
APPLICANT: Arvanitakis, Leandros
APPLICANT: Arvanitakis, Leandros
APPLICANT: Arvanitakis, Leandros
APPLICANT: Arvanitakis, Leandros
APPLICANT: Mesri, Enrique
TITLE OF INVENTION: KSHV POSITIVE CELL LINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: BRAWAN, SUSAN J.
RECISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08728603; Patent No. 6093806; GENERAL INFORMATION: APPLICANT: Cesarman, Ethel
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US-09-371-772B-5737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73, Application US/09433699B
Patent No. 6165786
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. COWSET
TILLS OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REPERENCE: RTS-0109
CURRENT PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 73
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED HERPESVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.1%; Score 12; DB 3; Length 20; Best Local Similarity 75.0%; Pred. No. 1.1e+04; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                AUDICESSES:
AUDICESSES:
CIINTON SQUARE, DEVIND & LOIDE
CITY:
CITY:
COUNTRY: USA
ZIP: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/08/728,603
FLING DATE: 10-CT-1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 19603/720
TELERPHONE: 716-26-1600
TELERPHONE: 716-26-1600
                                                     NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEB: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 58.1%; Score 12.2; DB 3; al Similarity 82.4%; Pred. No. 9.1e+03; 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-699-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TGGCGTATCTGAAGAGTCTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGAGCTAAAGAGTCTG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserva
                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-433-699-73/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-728-603-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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APPLICANT: Struck, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Besobedod, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions RO
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT PAPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1995-08-10
PRIOR FILING DATE: 1995-01-026
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFFWARE: PatentIn version 3.0
SEQ ID NO 5737
LENTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5737, Application US/10138674B

Sequence 5737, Application US/10138674B

Patent No. 7034009

GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Bavco, Pam APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: WIDMER: US/10/138,674B
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5737
LENGTH: 16
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Pred. No. 1.4e+04;
2; Mismatches 2; Indels
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US-09-371-772B-5737
Sequence 5737, Application US/09371772B
PRETENT NO. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/07852260; Patent No. 5525715; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%;
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Best Local Similarity 73.3
Matches 11; Conservative
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Best Local Similarity 73.3'
Matches 11; Conservative
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US-10-138-674B-5737
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APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: rc-lus/ma-lus
OPERATING SYSTEM: rc-lus/ma-lus
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILLING DATE: 19920619
CILLSSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAMM: White, John P.
REGISTRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 3677-9550
TELEPRATION INFORMATION:
TELEPRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 36607-B-PCT-US
TELEPRATION NUMBER: 317-9550
TELEPRATION NUMBER: 317-9550
TELEPRATION NOW 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/07936421
Sequence 18, Application US/07936421
Patent No. 5750390
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Aemeth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATWENT OF DISEASES CAUSED
TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
COUNTRY: USA
COUNTRY: USA
ICOMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM COmpatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DALECTLE TYPE: DNA (genomic)
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Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
HATI-SENSE: NO
US-07-852-260-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-07-936-421-18
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sequence 1002932, Sequence 1227779, Sequence 1410057, Sequence 376212,

Sequence Sequence Sequence Sequence

Sequence

US-10-310-914A-1058239 US-11-083-784-276438 US-11-083-784-276470 US-11-083-784-36530 US-11-083-784-825601 US-11-083-784-825591 US-11-083-784-1002832 US-11-083-784-1002832 US-11-083-784-11002332 US-11-083-784-1410057 US-11-101-244-276438 US-11-101-244-276438 US-11-101-244-276438 US-11-101-244-1002932 US-11-101-244-1002932 US-11-101-244-1002932 US-11-101-244-110057 US-11-013-114A-376212 US-11-013-144-136384 US-11-01-244-136384

Sequence

1227779,

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

Sequence

1330360, 252928,

Sequence

1368384

Sequence 2 Sequence 2 Sequence 1

Sequence Sequence

US-10-310-914A-566703

ALIGNMENTS

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GENERAL INCURATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Beake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 277064
LEMENTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 277064, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUGGCCUAUCUGAAGA 19
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Best Local Similarity 68.8
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-083-784-277064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-083-784-277064
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Sequence 277064,
Sequence 134779,
Sequence 136838,
Sequence 880853,
Sequence 880856,
Sequence 1324693,
Sequence 252899,
Sequence 252899,
Sequence 346041,
Sequence 346141,
Sequence 346141,
Sequence 346141,
Sequence 346141,
Sequence 346141,
Sequence 346141,
                                                                                                       June 9, 2006, 00:20:20; Search time 848 Seconds (without alignments) 304.293 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-083-784-277064
US-11-101-244-277064
US-10-310-914A-1347779
US-10-310-914A-1367779
US-11-083-784-252899
US-11-083-784-80853
US-11-083-784-1324693
US-11-101-244-880956
                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
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                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
                                                                                                                                                                            US-09-743-825-8
21
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Maximum DB seq length: 21
                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                                                                                                             Sequence:
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                                                                                                            Run on:
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Gaps

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Indels

Score 14.4; DB 14; Pred. No. 5.1e+03; 1; Mismatches 1;

16

Length 19;

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Gaps
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Pred. No. 6.5e+03;
6; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                           Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dharmacon, Inc.
APPLICANT: Ethorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Ascaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NOS 252899
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: KNOTOVA, Anastasia
APPLICANT: KNOTOVA, Anastasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 11;
Pred. No. 6.5e+03;
0; Mismatches 3;
   CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ 1D NOS: 1388402 SOFWARE: Patentin version 3.3 SEQ ID NO 1368338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 880853, Application US/11083784; Publication No. US20050245475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-083-784-252899
; Sequence 252899, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US/10/714,333
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52.6%;
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al Similarity 84.2%;
16; Conservative
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Best Local Similarity 52.6'
Matches 10; Conservative
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CRGANISM: Homo sapiens
US-11-083-784-252899
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 ; ORGANISM: Human
US-10-310-914A-1368338
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Publication No. US20060003322A1

GENERAL INCRMATION.

APPLICANT: Bentwich, Isaac

APPLICANT: Bhiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNMERE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 1347779
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Publication No. US20060003322A1
Reblication No. US2006000332A1
Republication No. US2006000332A1
Republication No. US2006000332A1
Republication No. US2006000332A1
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Republican: Shiler, Kvuzat
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68.6%; Score 14.4; DB 15; Length 19;
Best Local Similarity 68.8%; Pred. No. 5.1e+03;
Matches 11; Conservative 4; Mismatches 1; Indels
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                                                                                        APPLICANT: Characon, Inc.
APPLICANT: Rhvorova, Anastasia
APPLICANT: Rhvorova, Anastasia
APPLICANT: Responded, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 277064
Sequence 277064, Application US/11101244
Publication No. US20050246794A1
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4 CUGGCCUAUCUGAAGA 19
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Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-277064
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                                   Publication No. US20
GENERAL INFORMATION:
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ORGANISM: Human
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Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
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ORGANISM: Homo sapiens
US-11-083-784-1324693
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US-11-101-244-252899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
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j Sequence 880-880.56

j Sequence 880-86.70

j Publication No. US202050245475A1

j GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

j APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

TITLE OF INVENTION Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT PILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PLING DATE: 2003-11-14

PRIOR PLING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENTH: 19
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Leake, Devin
    APPLICANT: Marshall, William
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
    FILE REFERENCE: 13499US
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Pred. No. 6.5e+03;
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Best Local Similarity 57.9%; Pred. No. 6.5e
Matches 11; Conservative 5; Mismatches
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 880853
LENGTH: 19
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1 UGAUGAAUCUGAAGAGUCU 19
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                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA; ORGANISM: Homo sapiens
US-11-083-784-880853
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US-11-083-784-880956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Ansthall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOPTWARE: Proprietary
SEQ ID NO 252899
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
IIILE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 14;
Pred. No. 6.5e+03;
6; Mismatches 3;
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Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3;
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 1324693
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Publication No. US20050246794A1
GENERAL INFORMATION:
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Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 346041

Sequence 346041, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: RAVOROVA, Anastasia
APPLICANT: Rewnolds, Angela
APPLICANT: Rewnolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITLE OF INVERTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SOFTWARE: Proprietary
INWERN OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                             Indels
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Publication No. US2005024547541
GENERAL INFORMATION:
APPLICANT: Dharmora, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 15;
Pred. No. 6.5e+03;
6; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR PILING DATE: 2002-01-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                67.6%;
52.6%;
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1 UUGAGUAUCUGAAGAGU 17
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Best Local Similarity 52.6'
Matches 10; Conservative
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Best Local Similarity 58.8'
                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1324693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-11-083-784-346041
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US-11-083-784-346141
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Pred. No. 6.5e+03;
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GENERAL INFORMATION: USZUDOZ46/794A1

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Responds, Angela

APPLICANT: Responds, Stephen

APPLICANT: Beake, Devin

APPLICANT: Responds, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 880956
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Darmacon, Inc.
; APPLICANT: RAyrolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.6%; Score 14.2; DB 15;
ilarity 57.9%; Pred. No. 6.5e+03;
Conservative 5; Mismatches 3;
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                  CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SEQ ID NO 880853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 880956, Application US/11101244; Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TGGCGTATCTGAAGAGTCT 20
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1 UGAUGAAUCUGAAGAGUCU 19
                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-880853
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; ORGANISM: Homo sapiens
US-11-101-244-880956
  FILE REFERENCE: 13499US
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Publication No. US2050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respirate, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICANT: Ascaringe, Stephen
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07

PRIOR PLILING DATE: 2003-01-07

PRIOR PLILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 2003-01-07

PRIOR PRIOR PRIOR DATE: 2003-01-07

PRIOR PRIOR PRIOR PRIOR NUMBER: 2003-01-07
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
SOFTWARR: PROPICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARR: PROPICEATY
SEQ ID NO 346141
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1 UUGAGUAUCUGAAGAGU 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-346141
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; ORGANISM: Homo sapiens
US-11-101-244-346041
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: | |:|:||||||: Db 1 UUGAGUAUCUGAAGAGU 17 Search completed: June 9, 2006, 00:36:01 Job time : 848 secs (0108N) YUD18 860d SILL,

us-09-743-825-8.rnpbn

- nucleic search, using sw model

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Run on:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

253354 seqs, 63461778 residues

ctggcgtatctgaagagtctg 21 IDENTITY NUC Gapop 10.0 , Gapext 1.0

US-09-743-825-8 21

Title: Perfect score:

Sequence:

Scoring table:

Searched:

Length DB ID Description 17 6 US-10-514-776-361 Sequence 361 19 6 US-10-514-776-361 Sequence 56, 20 6 US-10-518-256 Sequence 56, 21 6 US-10-518-258 Sequence 52, 21 6 US-10-518-258 Sequence 22, 21 7 US-11-251-465-303 Sequence 137 19 7 US-11-251-465-303 Sequence 137 19 7 US-11-251-465-503 Sequence 137 19 7 US-11-251-465-504 Sequence 504 21 7 US-11-251-465-504 Sequence 10, 21 7 US-11-251-465-504 Sequence 10, 21 7 US-11-251-465-504 Sequence 10, 21 7 US-11-251-465-504 Sequence 50, 21 7 US-11-291-697-503 Sequence 50, 21 7 US-11-291-697-503 Sequence 50, 21 7 US-11-291-697-5003 Sequence 50, 20 7 US-11-291-491-391 Sequence 50, 20 7 US-11-204-427-31 Sequence 31, 20 7 US-11-21-465-588 Sequence 588 19 7 US-11-251-465-588 Sequence 769 19 7 US-11-251-465-769 Sequence 769 19 7 US-11-251-465-7			de			SUMMERTES	
11.8 56.2 17 6 US-10-514-776-361 Sequence 36. 10.8 51.4 19 6 US-10-934-215-56 Sequence 56. 10.2 48.6 20 6 US-10-531-832-58 Sequence 22. 10.2 48.6 21 7 US-11-251-465-460 Sequence 27. 10.2 48.6 21 7 US-11-251-465-460 Sequence 27. 10.47.6 19 7 US-11-251-465-503 Sequence 57. 10 47.6 19 7 US-11-251-465-503 Sequence 503. 10 47.6 20 7 US-11-251-465-503 Sequence 503. 10 47.6 21 7 US-11-251-465-504 Sequence 10. 47.6 21 7 US-11-251-465-504 Sequence 10. 10 47.6 21 7 US-11-251-465-504 Sequence 54. 10 47.6 21 7 US-11-251-465-504 Sequence 54. 10 47.6 21 7 US-11-251-465-504 Sequence 50. 10 47.6 21 7 US-11-251-465-504 Sequence 54. 10 44.8 20 6 US-10-511-937-2085 Sequence 37. 10 44.8 20 6 US-10-511-937-2085 Sequence 36. 10 44.8 20 7 US-11-21-465-588 Sequence 38. 10 7 US-11-21-465-588 Sequence 38. 10 7 US-11-21-465-588 Sequence 38. 10 7 US-11-21-465-588 Sequence 58. 10 7 US-11-21-465-588 Sequence 76. 10 8. 10 7 US-11-21-465-588 Sequence 76. 10 8. 10 7 US-11-21-465-588 Sequence 76. 10 8. 10 7 US-11-21-465-769 Sequenc	Mo.	Score	Query Match		DB	ID	Description
10.8 51.4 19 6 US-10-994-215-56 Sequence 56, 10.2 48.6 20 6 US-10-539-228 Sequence 22, 10.2 48.6 21 7 US-11-832-28 Sequence 22, 10.2 48.6 21 7 US-11-251-465-460 Sequence 27, 10.4 7.6 19 7 US-11-251-465-503 Sequence 27, 10.4 7.6 19 7 US-11-251-465-503 Sequence 513, 10.4 7.6 20 7 US-11-251-465-503 Sequence 510, 47.6 21 7 US-11-251-465-504 Sequence 510, 47.6 21 7 US-11-271-280-280-503 Sequence 510, 47.6 21 7 US-11-281-484-2 Sequence 510, 47.6 21 7 US-11-281-465-587 Sequence 510, 47.6 21 7 US-11-291-697-503 Sequence 510, 47.6 20 7 US-11-291-45-587 Sequence 510, 47.6 20 7 US-11-291-45-588 Sequence 31, 44.8 20 7 US-11-204-427-36 Sequence 38, 59.4 44.8 20 7 US-11-204-427-36 Sequence 588, 59.4 44.8 20 7 US-11-204-427-36 Sequence 588, 59.4 44.8 20 7 US-11-21-465-588 Sequence 545, 59.5 59.5 59.5 59.5 59.5 59.5 59.5 59	-	11.8	56.2	17	و ا	US-10-514-776-361	Seguence 361, App
10.2 48.6 20 6 US-10-511-832-58 Sequence 58, 10.2 48.6 21 6 US-10-539-032-22 Sequence 22, 10.2 48.6 21 6 US-10-539-032-22 Sequence 22, 10.2 48.6 21 7 US-11-251-465-460 Sequence 277, 10.4 7.6 19 7 US-11-158-209-277 Sequence 137, 10.4 7.6 19 7 US-11-251-465-503 Sequence 503, 10.4 7.6 20 7 US-11-251-465-240 Sequence 503, 10.4 7.6 21 7 US-11-251-465-240 Sequence 504, 10.4 7.6 21 7 US-11-251-465-240 Sequence 504, 10.4 7.6 21 7 US-11-251-465-504 Sequence 504, 10.4 7.6 21 7 US-11-251-465-504 Sequence 10, 10.4 7.6 21 7 US-11-251-465-504 Sequence 504, 10.4 7.6 21 7 US-11-251-465-504 Sequence 504, 10.4 7.6 21 7 US-11-251-465-504 Sequence 507, 10.4 7.6 21 7 US-11-251-465-504 Sequence 507, 10.4 7.6 21 7 US-11-231-697-503 Sequence 507, 10.4 44.8 20 6 US-10-511-832-45 Sequence 33, 10.4 44.8 20 7 US-11-204-427-33 Sequence 33, 10.4 44.8 20 7 US-11-204-427-34 Sequence 38, 10.4 44.8 20 7 US-11-204-427-34 Sequence 588, 10.4 44.8 20 7 US-11-21-465-588 Sequence 588, 10.4 44.8 20 7 US-11-21-465-588 Sequence 588, 10.5 11.2 11.2 11.2 11.2 11.2 11.2 11.2 11	0	10.8	51.4	19	9	US-10-994-215-56	56. 3
10.2 48 6 21 6 US-10-599-032-22 Sequence 22, 10.2 48.6 21 7 US-11-251-465-460 Sequence 460, 10.2 47.6 11 7 US-11-251-465-137 Sequence 460, 10 47.6 19 7 US-11-251-465-503 Sequence 137, 10 47.6 19 7 US-11-251-465-503 Sequence 137, 10 47.6 20 7 US-11-251-465-240 Sequence 240, 10 47.6 21 7 US-11-251-465-504 Sequence 240, 10 47.6 21 7 US-11-251-465-504 Sequence 240, 10 47.6 21 7 US-11-251-465-504 Sequence 10, 10 47.6 21 7 US-11-251-465-504 Sequence 10, 10 47.6 21 7 US-11-251-465-504 Sequence 10, 10 47.6 21 7 US-11-264-029-10 Sequence 503, 10 47.6 11 7 US-11-291-697-5436 Sequence 500, 10 47.6 11 8 7 US-11-291-697-503 Sequence 500, 10 44.8 20 6 US-10-511-832-45 Sequence 500, 10 44.8 20 6 US-10-511-832-45 Sequence 33, 10 44.8 20 7 US-11-204-427-33 Sequence 34, 10 44.8 20 7 US-11-204-427-34 Sequence 38, 10 4 44.8 20 7 US-11-21-465-58 Sequence 588, 10 4 44.8 20 7 US-11-21-464-27-34 Sequence 38, 10 4 44.8 20 7 US-11-21-465-58 Sequence 588, 10 4 44.8 20 7 US-11-21-465-58 Sequence 588, 10 4 44.8 20 7 US-11-21-465-58 Sequence 769, 10 44.8 20 7 US-11-21-465-769 Sequence 769, 1	ო	10.2	48.6	20	9	US-10-511-832-58	58,
10.2 48.6 21 7 US-11-251-465-460 Sequence 460. 10 47.6 19 7 US-11-121-465-137 Sequence 277, 10 47.6 19 7 US-11-251-465-137 Sequence 1377, 10 47.6 19 7 US-11-251-465-137 Sequence 137, 10 47.6 20 7 US-11-251-465-503 Sequence 106, 10 47.6 21 7 US-11-251-465-240 Sequence 503, 10 47.6 21 7 US-11-251-465-504 Sequence 540, 10 47.6 21 7 US-11-251-465-504 Sequence 540, 10 47.6 21 7 US-11-251-465-504 Sequence 10, 10 47.6 21 7 US-11-251-465-504 Sequence 10, 10 47.6 21 7 US-11-231-451-50 Sequence 500, 10 47.6 21 7 US-11-231-251-251 Sequence 510, 10 47.6 21 7 US-11-231-251-251 Sequence 510, 10 47.6 21 7 US-11-231-451 Sequence 510, 10 44.8 20 6 US-10-511-937-2085 Sequence 208, 10 4 44.8 20 7 US-11-251-465-587 Sequence 33, 10 4 44.8 20 7 US-11-204-427-36 Sequence 38, 10 4 44.8 20 7 US-11-204-427-36 Sequence 38, 10 4 44.8 20 7 US-11-21-465-588 Sequence 588, 10 4 44.8 20 7 US-11-21-465-588 Sequence 588, 10 4 44.8 20 7 US-11-21-465-588 Sequence 588, 10 7 US-11-21-465-588 Sequence 769, 10 511-251-465-769 Sequence 769, 10 511-	4	10.2	48.6	21	ø	US-10-539-032-22	22
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9.4 44.8 20 6 US-10-511-832-45 Sequence 45, 9.4 44.8 20 7 US-11-204-427-36 Sequence 33, 9.4 44.8 20 7 US-11-204-427-36 Sequence 36, 9.4 44.8 20 7 US-11-204-427-36 Sequence 36, 9.4 44.8 21 7 US-11-21-465-588 Sequence 38, 9.2 43.8 19 7 US-11-251-465-769 Sequence 7898, 9.2 43.8 19 7 US-11-251-465-769 Sequence 7898, 9.2 43.8 19 7 US-11-251-465-769	18	4.0	44.8	20	9	US-10-511-937-2085	
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9.4 44.8 20 7 US-11-204-427-38 Sequence 38, 9.4 44.8 21 7 US-11-251-465-588 Sequence 588, 9.2 43.8 19 7 US-11-251-465-769 Sequence 769, 9.2 43.8	21	9.4	44.8	20	7	US-11-204-427-36	36,
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STIMMARTES

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US-10-994-215-56

Sequence 56, Application US/10994215

Sequence 56, Application US/10994215

Publication No. US20060111302A1

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APPLICANT: The Scripps Research Institute

TILE OF INVEXTION: COMPOSITIONS AND METHODS TO REDUCE MUTAGENESIS

TILE REFERENCE: 91-0001100S

CURRENT APPLICATION NUMBER: US/10/994,215

CURRENT PILING DATE: 2004-11-19

NUMBER OF SEQ ID NOS: 74

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RESULT 5

US-11-251-465-460/c

US-11-251-465-460/c

Sequence 460, Application US/11251465

Publication No. US20060094061A1

GENERAL INFORMATION:

APPLICANT: Brys, Reginald

APPLICANT: Tomme, Peter

APPLICANT: Tomme, Peter

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TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE TILING DATE: 2005-10-14

CURRENT APPLICATION NUMBER: US/11/251,465

CURRENT ELING DATE: 2006-10-14

PRIOR APPLICATION NUMBER: 60/619,384
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Sequence 277, Application No. US2006008852A1
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APPLICANT: Thomas Gassenmeier
APPLICANT: Thomas Gassenmeier
APPLICANT: Thomas Gassenmeier
APPLICANT: Marcus Conradt
APPLICANT: 
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48.6%; Score 10.2; DB 7;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 3;
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SOFWARE: Patentin version 3.3
SEQ ID NO 460
LENGTH: 21
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TITLE OF INVENTION: Glucose and/or fructose transporter 'NaGLT1' and gene thereof
FILE REPERENCE: 4439-4034
CURRENT APPLICATION NUMBER: US/10/539,032
CURRENT FILING DATE: 2005-06-13
PRIOR APPLICATION NUMBER: JP P2002-363014
PRIOR PILIATION DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENT OF 2.1
LENGTHARE: PATENT OF 2.2
LENGTHARE: PATENT OF 2.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/10511832
Publication No. US20060105973A1
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION
TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION
TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/511,832
CURRENT PILING DATE: 2004-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
                                                                                                                                                                                                                                                   Query Match 51.4%; Score 10.8; DB 6; Length 19; Best Local Similarity 85.7%; Pred. No. 2.3e+03; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.6%; Score 10.2; DB 6; Length 20; Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 12; Conservative 0; Mismatches 3; Indels
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; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FRATURE:
; OTHER INFORMATION: synthetic oligonucleotide primer US-10-994-215-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-511-832-58
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; Sequence 22, Application US/10539032
; Publication No. US20060116505A1
; GENERAL INFORMATION:
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Best Local Similarity 80.0
Matches 12; Conservative
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P254@FIC.
CURRENT APPLICATION NUMBER: US/11/296,092
CURRENT PLOATION NUMBER: US/09/866,028
FRIOR APPLICATION NUMBER: US/09/866,028
FRIOR PADLICATION NUMBER: US/09/334
FRIOR PALING DATE: December 3, 1997
FRIOR PAPLICATION NUMBER: 60/069,334
FRIOR PAPLICATION NUMBER: 60/069,334
FRIOR PAPLICATION NUMBER: 60/069,238
FRIOR PILING DATE: December 11, 1997
FRIOR PILING DATE: December 11, 1997
FRIOR PILING DATE: December 11, 1997
FRIOR PILING DATE: December 12, 1997
FRIOR PILING DATE: December 16, 1997
FRIOR PILING DATE: December 17, 1997
FRIOR PILING DATE: December 17, 1997
FRIOR FILING DATE: DECEMBER 16, 1997
FRIOR FILING DATE: DECEMBER 16, 1997
FRIOR FILING DATE: DECEMBER 17, 1997
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
47.6%; Score 10; DB 7; I
Best Local Similarity 72.2%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 5;
                                                                                                                                                                                                       Sequence 106, Application US/11296092
Publication No. US20060105427A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul
Grimaldi, Christopher
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard, Audrey
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Hillan, Kenneth
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Napier, Mary
Roy, Margaret
Tumas, Daniel
                    3 GAAGAGTCTG 12
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                                                                                                                                                                      US-11-296-092-106
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                   | Sequence 177, Application US/11251465 | Sequence 177, Application US/1251465 | Publication No. US20060094061A1 | Sequence 177, Application No. US20060094061A1 | Sequence 177, Application No. US20060094061A1 | Sequence 177, Applicant No. US20060094061A1 | Septicant No. USACHATION: Reginal APPLICANT: Vandeghinste, Nick APPLICANT: Tomme, Peter | APPLICANT: Klaassen, Hubertus | TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The TITLE OF INVENTION: Inflammatory Diseases | TITLE OF INVENTION: Inflammatory Diseases | TITLE OF INVENTION: UNMER: US/11/251,465 | CURRENT FILING DATE: 2005-10-14 | PRIOR PILICATION NUMBER: 2004-10-15 | NUMBER OF SEQ ID NOS: 880 | SOFTWARE: Patentin version 3.3 | SOFTWARE: Patentin version 3.3 | SEQ ID NO 137 | LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VS-11-251-465-503

VS-11-251-465-503

Sequence 503, Application US/11251465

Publication No. US20060094061A1

Sequence 503, Application US/11251465

Publication No. US20060094061A1

APPLICANT: Brys, Reginald

APPLICANT: Vandespinate, Nick

APPLICANT: Tomme, Peter

APPLICANT: Vandespinate, Nick

APPLICANT: Vandespinate, Nick

APPLICANT: Modeconinate, Nick

APPLICANT: Modeconinate, Nick

APPLICANT: Modeconinate, Nick

APPLICANT: None, Peter

APPLICANT: None, Peter

APPLICANT: Nick

APPLICANT: Nic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Knock-down target sequence US-11-251-465-137
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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Matches 10; Conservative
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10 CTGAAGAGTC 1
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Query Match 47.6%; Score 10; DB 7; Length 21; Best Local Similarity 72.2%; Pred. No. 6.2e+03; Matches 13; Conservative 0; Mismatches 5; Indels
  APPLICANT: Albig, Allan R.
TITLE OF INVENTION: Fibulin-3 and Uses Thereof;
FILE REFERENCE: 2879-109
CURRENT APPLICATION NUMBER: US/11/267,942
CURRENT FILING DATE: 2005-11-04
PRIOR APPLICATION NUMBER: 60/625,598
PRIOR APPLICATION NUMBER: 60/625,598
PRIOR PILING DATE: 2004-11-04
PRIOR PILING DATE: 2005-06-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial
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Sequence 504, Application US/11251465

Bublication No. US20060094061A1

Sequence 504, Application US/11251465

Bublication No. US20060094061A1

APPLICANT: Brys, Reginald

APPLICANT: Vandeghinate, Nick

TITLE OF INVENTION: Dolecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Inflammatory Diseases

CURRENT FILING DATE: 2005-10-14

PRIOR APPLICATION NUMBER: US/11/251,465

CURRENT FILING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOFTWARE PatentIn Version 3.3

SEQ ID NO SO4

LENGTH: 21
                                                                                            TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And TITLE OF INVENTION: Inflammatory Diseases

FILE OF INVENTION: Inflammatory Diseases

CURRENT PRILING DATE: 10/11/251,465

CURRENT PRILING DATE: 2005-10-14

PRIOR APPLICATION NUMBER: 60/619,384

PRIOR FILING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOFTWARE: Patentin version 3.3

SEQ ID NO 2.40

LENGTH: 21
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47.6%; Score 10; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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47.6%; Score 10; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Knock-down target sequence US-11-251-465-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Knock-down target sequence US-11-251-465-504
                        Vandeghinste, Nick
Tomme, Peter
Klaassen, Hubertus
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Brys, Reginald
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                                                   APPLICANT:
APPLICANT:
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Sequence 10, Application US/11264029
Publication No. US20060099171A1
GENERAL INFORMATION:
APPLICANT: University of Pennsylvania
TITLE OF INVENTION: mCITRL IS COSTIMULATORY FOR T CELLS
FILLE REFREENCE: P-8296-US
CURRENT APPLICATION UNMBER: US/11/264,029
CURRENT APPLICATION UNMBER: 2005-11-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.3
SEQ ID NO 10
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.6%; Score 10; DB 7; Length 21; Best Local Similarity 72.2%; Pred. No. 6.2e+03; Matches 13; Conservative 0; Mismatches 5; Indels
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Sequence 5436, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: NOVEL full length CDNA

FILLE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR PILICATION NUMBER: US/10/108,260

PRIOR PILICATION DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5436

LENGTH: 18
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RESULT 12
US-11-267-942-10/c
Sequence 10, Application US/11267942
Publication No. US20060094054A1
GENERAL INFORMATION:
APPLICANT: Schiemann, William P.

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US-LI-283-4484-2

JUNEAL-1283-4484-2

Sequence 2 Application US/11283484A

Publication No US20060115461A1

GENERAL INPORMATION:

APPLICANT: Debaracon, Inc.

APPLICANT: Robertson, Barbara

APPLICANT: Robertson, Kathryn

APPLICANT: Robertson, Kathryn

APPLICANT: Marshall, William S.

TITLE OF INVENTION: APPRARUS AND SYSTEM HAVING DRY GENE SILENCING COMPOSITIONS

FILE REPERENGE: Attorney Docket No. 16542.1

TITLE OF INVENTION NUMBER: 60/630320

PRIOR FILING DATE: 2005-11-18

PRIOR FILING DATE: 2005-11-18

PRIOR FILING DATE: 2005-04-11-22

PRIOR FILING DATE: 2005-05-04

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 2

LENGTH: 19

TYPE: DRA

ORGANISM: Homo sapiens

FRATURE:

FRATURE:

FRATURE:

NAME/KEY: misc_feature

COTHER INFORMATION: SIRNA targeting a SRD5al gene

US-11-283-484A-2

    TYPE: DNA
    ORGANISM: Artificial Sequence
    FRATURE:
    OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
    US-11-293-697-5436

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46.7%; Score 9.8; DB 7; Length 18;
Best Local Similarity 84.6%; Pred. No. 7.78+03;
Matches 11; Conservative 0; Mismatches 2; Indels
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46.7%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 7.7e+03;
Matches 11; Conservative 0; Mismatches 2; Indels
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US-11-283-484A-2
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Search completed: June 9, 2006, 00:36:32 Job time : 25 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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PAT 12-JUN-2003
        AX207008 Sequence
AX333519 Sequence
CS005340 Sequence
161735 Sequence 28
AX61711392 Sequence
AX64674 Sequence
AX734679 Sequence
AX734679 Sequence
AX730020 Sequence
AX130020 Sequence
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AX130020 Sequence
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AX378663 Sequence
AX70943 Sequence
AX778663 Sequence
AX778663 Sequence
AX77867 Sequence
AX77867 Sequence
AX37867 Sequence
AX37868 Sequence
AX378663 Sequence
AX378663 Sequence
AX378663 Sequence
AX37867 Sequence
AX37867 Sequence
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1 (bases 1 to 20)

Griffals,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 2812 06-MAY-2003;
Genset, S.A.;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 15-DEC-2004
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PA
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Sequence 2012 from patent US 6559294.
AR312275
AR312275.1 GI:31705701
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Sequence 48 from patent US 6828151.
AR614263.1 GI:56670377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .20
/organism="unknown"
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CS015023
AX207008
AX207008
AX353119
CS005340
CS005340
AX35322
AX33629
AX131002
AX5130020
AX130020
AX130020
AX130020
AX130020
AX278659
AX270943
AX313002
CQ88999533
CQ8899953
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Best Local Similarity 88.2
Matches 15; Conservative
Unknown.
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AR312275
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AR614263/c
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ACCESSION
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KEYWORDS
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ORGANISM
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AUTHORS
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ORIGIN
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AR654263 Sequence
AR653611 Sequence
AR096404 Sequence
BD217452 Antisense
AR031610 Sequence
AR011072 Sequence
AR152833 Sequence
AR152833 Sequence
AX755344 Sequence
AX755065 Sequence
AX755065 Sequence
AK15283 Sequence
AK16183 Sequence
B10136 PCR primer
DD200317 RNA Inter
                                                         9, 2006, 00:36:46; Search time 1983 Seconds (without alignments) 644.956 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                               6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR312275
AR614263
AR614263
AR614264
AR096404
BD217452
AR633610
AR03152833
BD134289
AX735344
AX759065
AK759065
AK759136
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                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1: gb_env:*
2: gb_pat:*
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Match
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Unknown. Unknown.

DD200470 AR023697 CS014609

DD200317

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13.8 12.2.2 12.2.2 12.2.2 12.2.2 12.2.2 1

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OS Unidentified
PN JP 2002519015-A/75
PN JP 2002519015-A/75
PP 02-4UL-2002
PP 17-4UN-1999 JP 2000557265
PR 26-4UN-1998 US 09/106038
PI BRENDA F BAKER, LEX M COWSERT
PC C1201/68,
CC Strandedness: Single,
CC Strandedness: Single,
CC Topology: Linear;
CC Antisense modulation of TNFR1 expression
FH Key Location/Qualifiers
FT source 1.18
FT Source (Organism='Unidentified'.
                                                                                                                                                                                  PAT 17-JUL-2003
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                                     Gaps
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Reder,J.N., Schatzman,R.C. and Tsuchihashi,Z.
Reder,J.N., Schatzman,R.C. and Tsuchihashi,Z.
Methods and compositions for diagnosis and treatment of iron
misregulation diseases
Patent: US 6849399-A 11 01-FEB-2005;
Bio-Rad Laboratories, Inc.; Hercules, CA
Location/Qualifiers
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     Length 18
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                                   3; Indels
                                                                                                                                                                                                               BD217452
BD217452.
JP 2002519015-A/75.
unidentified
unidentified
unidassified sequences.
unclassified sequences.
Baker, B.F. and Cowsert, L.M.
Antisense modulation of TWFR1 expression Patent: JP 2002519015-A 75 02-JUL-2002;
ISIS PHARMACEUTICALS INC
   61.0%; Score 12.2; DB 2;
82.4%; Pred. No. 8.3e+04;
ive 0; Mismatches 3;
                                                                                                                                                                                 BD217452 18 bp DNA
Antisense modulation of TNFR1 expression.
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Sequence 11 from patent US 6849399.
AR633610
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                                                                   4 CGCATAGACTTCTCAGA 20
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                                   14; Conservative
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                Best Local Similarity
Matches 14; Conserv
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     Query Match
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ACCESSION
VERSION
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BD217452/c
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TITLE
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AUTHORS
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AR633610
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           1 (bases 1 to 20)
Borchers, A.H. and Dobie, K.W.
Antisense modulation of hematopoietic cell protein tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM Unknown.
Unclassified.
Unclassified.
SE 1 (bases 1 to 20)
RS Peder, JN., Schatzman, R.C. and Tsuchihashi, Z.
Amethods and compositions for diagnosis and treatment of iron misregulation diseases
NAL Patent: US 6849399-A 12 01-FEB-2005;
Bio-Rad Laboratories, Inc.; Hercules, CA
Location/Qualifiers
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66.0%; Score 13.2; DB 2;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3;
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Baker, B.F. and Cowsert, L.M.
Antisense inhibition of TNFR1 expression
Patent: US 6007995-A 75 28-DEC-1999;
Location/Qualifiers
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                                                           expression
Patent: US 6228151-A 48 07-DEC-2004;
ISIS Pharmaceuticals, Inc.; Carlsbad,
Location/Qualifiers
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AR096404
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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Best Local Similarity 78.9°
Matches 15; Conservative
Unclassified.
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Unclassified.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 934 27-MAR-2003;
Molecular Engines Laboratories (FR)
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                                                                                                                                                    other sequences; artificial sequences.

1 (bases 1 to 20)
Sidlanski, D.
Sidlanski, D.
Detection of neoplasia by analysis of saliva
Detection of neoplasia by analysis of saliva
Patent: JP 2002505888-A 113 26-FEB-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS ARTIFICIAL Sequence
PN JP 2002505888-A/113
PP 10-MAR-1999 JP 2000535774
PR 10-MAR-1999 US 09/038637
PR 10-MAR-1998 US 09/038637
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                                        linear
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Detection of neoplasia by analysis of saliva.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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                                                                  BD134289
BD134289.1 GI:33229234
JP 2002505888-A/113.
Synthetic construct
Synthetic construct
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AX735344.1 GI:30514621
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Unclassified.
1 (bases 1 to 20)
Polymeropoulos, M.H. and Merril, C.R.
Bleven highly informative microsatelite repeat polymorphic DNA markers
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                                                                              Query Match 61.0%; Score 12.2; DB 2; Length 20; Best Local Similarity 82.4%; Pred. No. 8.5e+04; Matches 14; Conservative 0; Mismatches 3; Indels
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Sequence 60 from patent US 5861504.
AR031072 AR031072.1 GI:5944286
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/wol_type="unassigned DNA"
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/mol_type="genomic DNA"
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Sidransky, D.
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Unclassified.
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1 (bases 1 to 18)

Komai,K., Kaneko,H. and Nakatsuka,I.
Oligonuclectide for use in checking presence or absence of mutation in human-derived cytochrome P450IIC18 gene
Patent: US 5821062-A 1 13-0CT-1998;
Location/Qualifiers
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CIGAGNUCLECTION TYPE GENE OF HUMAN DERIVED
CYTOCHROME PASOITS
PATELYING MUTATION TYPE GENE OF HUMAN DERIVED
CYTOCHROME PASOITS
PATENT: JP 1995285987-A 1 31-OCT-1995;
SUMITOMO CHEM CO LID
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PCR primer to amplify mutated genes encoding human cytochrome
P450IIC18.
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.location/Qualifiers
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Artificial sequences.
31-05T-1995
29-MAR-1994 JP 1994059386
KOMAI KOICHING, KANEKO HIDEO, NAKATSUKA IWAO
strandedness: Single;
                       linear
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86.7%; Pred. No. 1.4e+05;
tive 0; Mismatches 2; Indel8
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86.7%; Pred. No. 1.4e+05;
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/organism="unknown"
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                 Sequence 1 from patent US 5821062.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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B10136.1 GI:22026764
JP 1995285987-A/1.
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                    Unclassified.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Strosberg,A.D.
CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF
Patent: WO 9735973-A 8 02-OCT-1997;
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                                                                                                                                                                                                                                                                             Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                               AX759065 17 bp DNA Sequence 2386 from Patent W003040369. AX759065
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Location/Qualifiers
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Sequence 8 from Patent W09735973.
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RESULT 12 A65727

REFERENCE AUTHORS

KEYWORDS

TITLE JOURNAL

FEATURES

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RESULT 13

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L Patent: JP 2005517423-A 26 16-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
OS Artificial Sequence
PN JP 2005517423-A/26
PD 16-JUN-2005
PF 11-FEB-2003 JP 2003569157
PR 06-JUN-2002 US 60/358580, PR 15-JAN-2003 US 60/440129, 12-NOV-2002 US 60/358580, PR 15-JAN-2003 US 60/40293, 11-MAR-2002 US 60/353124, PR 29-AUG-2002 US 60/406784, 05-SEP-2002 US 60/408378 PI leonid bejelman, james mcswiggen
CC Description of Artificial Sequence: Target Sequence/siNA CC sense region
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RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta (siNA).
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DD20017.1 GI:85551394
DD2001517423-A/26.
Synthetic construct
synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 19)
Beigelman,L. and Mcswiggen,J.
RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta
(81NA)
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    .19
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Biocceleration Ltd. Biocceleration Ltd. earch time 2496 Seconds (without alignments) 448.072 Million cell updates/secresidues meters: 14588	cted by chance to have a score distribution. Description CO792214 NT014C A1 C2174208 MIAA-2511 C2174098 MIAA-2511 C2175608 MIAA-2511 C2175608 MIAA-2110 C217609 MIAA-2110 C217609 MIAA-2110 C217609 MIAA-2110 C217609 MIAA-2110 C217609 MIAA-3124 C2177809 MIAA-3124 C2177809 MIAA-3129 A3840659 Arabidops A2660128 1M0016623 C2177809 MIAA-3119
GenCore version right (c) 1993 - 2006 Barch, using sw model 9, 2006, 00:41:53; Sea 743-825-10 3catagacttctcaga 20 rY_NUC 10.0, Gapext 1.0 88 seqs, 27959665780 re atisfying chosen parame 0 20 20 20 20 20 20 20 20 20 20 20 20 2	est4:* est5:* est5:* est5:* est5:* est5:* est7:* est7:* est7:* est8:* es
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MIAA-26N17b.gl Meloidogyne incognita BAC end sequence library
(MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
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Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
                                                                                                                                    Chromadorea; Tylenchida; Tylenchina;
                                                                                                                                                                               (bases 1 to 14)
Mitreva,M., McCatrer,J.P., Pape,D., Martin,J., Mylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
                                                                                                                               Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tyl
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
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                                                                                      Meloidogyne incognita (southern root-knot nematode)
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Meloidogyne incognita
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/organism="Meloidogyne incognita"
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84.6%; Pred. No. 3.3e+06;
live 0; Mismatches 2;
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MIAA-25J15b.g1 Meloidogyne incognita BAC end sequence library (MIAASS 001) Meloidogyne incognita genomic, genomic survey sequence.
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(MIAAGSs 001)"
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Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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MAAA-3G17c.g1 Meloidogyne incognita BAC end sequence library (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
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Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1800
Fax: 314 286 1810
NotI-SalI site of pCMVSport6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 kB.
TAG_LIB=NT"
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Pred. No. 3.3e+06;
9; Mismatches 2; Indels
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Pred. No. 2.1e+06;
0; Mismatches 3;
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strain="Race 1"
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1 Similarity 80.0%;
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Class: BAC ends.
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/clone_lib="Meloidogyne incognita BAC end sequence library
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Meloidogyne incognita
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 14)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mittera M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: nemacode@watson.wustl.edu
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/mol_type="genomic DNA"
/strain="Race 1"
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CZ175608.1 GI:58343901
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CZI76205.1 GI:58344498
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         11; Conservative
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(MIAAGSS 001)"
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(MIAAGSS 001)"
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Meloidogyne incognita
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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BAC ends sequenced by Washington University Genome Sequencing Center Class: BAC ends.
Location/Qualifiers
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BAC ends sequenced by Washington University Genome Sequencing
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Contect: Mirrera M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 49.0%; Score 9.8; DB 13; Length 14; Best Local Similarity 84.6%; Pred. No. 3.3e+06; Matches 11; Conservative 0; Mismatches 2; Indels
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:6306"
/dev_stage="L2"
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Pred. No. 3.3e+06;
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/strain="Race 1"
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CZ174914.1 GI:58343207
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Meloidogyne incognita (southern root-knot nematode)
Meloidogyne incognita
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Pred. No. 3.3e+06;
0; Mismatches 2;
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Pred. No. 3.3e+06;
0; Mismatches 2;
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/strain="Race 1"
                            db_xref="taxon:6306"
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CZ178035.1 GI:58346328
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/clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 001)"
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MIAA-22K24b.gl Meloidogyne incognita BAC end sequence library
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Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
1 (basea, M., McCarter, J.P., Pape, D., Martin, J., Wylie, T.,
Clifton, S., Budiman, A., Lakey, N., Opperman, C. and Bird, D. McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."
  1 (bases 1 to 14)
Mitzeva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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BAC ends sequenced by Washington University Genome Sequencing
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BAC ends sequenced by Washington University Genome Sequencing
                                                                                                                                   Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
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Contact: Mirreva M
Washington University in St. Louis
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Fal: 314 286 1810
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Organism="Meloidogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9.8; DB 13;
Pred. No. 3.3e+06;
0; Mismatches 2;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 49.0%;
| Similarity 84.6%;
| 11; Conservative
                                                                               incognita
Unpublished (2005)
Contact: Mitreva M
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Best Local Similarity
Matches 11; Conserv
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/dev_stage="L2"
/clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 001)"
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/clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 001)"
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                                                                                                                  /note="Vector: pcUGI, Site_1: HindIII; Site_2: HindIII; Abc library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."
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Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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BAC ends sequenced by Washington University Genome Sequencing
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Contact: Mitreva Mitreva Mushington University in St. Louis
Washington University School of Medicine
Washington University School of Medicine
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Pax: 314 286 1800
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5

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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Jalsmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, 84112, USA
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Fax: 801 585 7177
Fax: 801 585 717
Fax: 801 
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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84.6%;
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                    (bases 1 to 19)
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(MIAAGSS 001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-SEP-2004) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Bry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (Inttp://www.genoplante.com and http://genoplante-info.info.iopiogen.fr).

Location/Qualifiers
                                                                                 AJ840659 18 bp DNA linear GSS 08-FEB-2006
Arabidopsis thallana T-DNA flanking sequence, right border, clone
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/note="T-DNA flanking sequence
right border"

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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
                                                                                                                                                                   genomic survey sequence.
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GSS.
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Balzergue, S.
Direct Submission
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chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
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                                                                                               Score 9.8; DB 11; Length 19;
Pred. No. 3.4e+06;
0; Mismatches 2; Indels
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|dev_stage="L2"
|/clone lib="Meloidogyne incognita BAC end sequence library
(MTAAGSS 001)"
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1M0538G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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(bases 1 to 20)
                     1 (bases 1 to 20)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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                                                                                                                                                       Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: nematode@wastson.wustl.edu
Email: nematode@wastson.wustl.edu
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Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Meloidogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00

Plate: 0538 row: G column: 04

Seq primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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AZ660128.1 GI:11797274
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Best Local Similarity 84.6
Matches 11; Conservative
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus (C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi] 4732114 [gb] AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Far: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
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                                                                                                                     organism="Mus musculus"
                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                      db_xref="taxon:10090"
clone="UUGC1M0538G04"
High quality sequence stop: 20.
Location/Qualifiers
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Unpublished (2005)
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9, 2006, 01:56:22

Search completed: June Job time: 2498 secs

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/clone lib="Mestor: DUGI; Site_1: HindIII; Site_2: HindIII;

/note="Vector: PUGI; Site_1: HindIII; Site_2: HindIII;

BAC library constructed by Arief Budiman and Nathan Lakey

at Orion Genomics, and David Bird and Charles Opperman at

Center for the Biology of Nematode Parasitism at NCSU."
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MIAA-3N19c.gl Meloidogyne incognita BAC end sequence library
(MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
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| Adv stage="L2"
|clone llb="Meloidogyne incognita BAC end sequence library
(MIAAGES 001)"
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Meloidogyne incognita
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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BAC ends sequenced by Washington University Genome Sequencing
Center
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Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
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Pred. No. 7e+06;
0; Mismatches 3; Indels
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Pred. No. 7e+06;
0; Mismatches 3; Indels
/organism="Meloidogyne incognita"
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/strain="Nace 1"
/db_xref="taxon:6106"

    16 Coganism="Meloidogyne incognita"
/mol type="genomic DNA"
/gtrain="Race 1"

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Location/Qualifiers
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CZ178031.1 GI:58346324
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1 Similarity 78.6%;
11; Conservative
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Matches 11; Conservative (
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Sequence 60, Appl
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Sequence 113, App
Sequence 113, App
Sequence 14, Appli
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Sequence 289, App
Sequence 4, Appli
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Sequence 1238, Ap
Sequence 1239, Ap
Sequence 35, Appl
Sequence 35, Appl
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Sequence 4697, Ap
Sequence 113, App
                                                                                                                         June 9, 2006, 01:14:56 ; Search time 99 Seconds (without alignments) 378.002 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-007-010-48
US-08-05-59-12
US-09-106-038A-75
US-09-20-559-11
US-07-922-723A-60
US-07-922-733A-60
US-07-952-277A-60
US-07-952-277A-60
US-08-37-113
US-08-319-912-8
US-08-119-912-8
US-08-119-912-8
US-08-291-932A-289
US-08-291-932A-289
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US-09-696-791-1238
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US-09-422-978-4697
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM nucleic - nucleic search, using sw model
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Match Length
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11.2 56.0 20 2 US-08-256-426B-113 Sequence 113, App 11.2 56.0 20 3 US-09-249-730-204 Sequence 204, App 11.2 56.0 20 3 US-09-249-730-264 Sequence 204, App 11.2 56.0 20 3 US-09-189-452-3144 Sequence 204, App 11.2 56.0 20 3 US-09-189-452-314 Sequence 204, App 11.2 56.0 20 3 US-09-194-204 Sequence 204, App 11.2 56.0 20 3 US-09-975-123-28 Sequence 204, App 11.2 55.0 18 3 US-09-544-398B-629 Sequence 205, App 11.2 55.0 18 3 US-09-543-771B-629 Sequence 205, App 11.5 5.0 18 3 US-09-543-771B-629 Sequence 205, App 11.5 5.0 20 3 US-09-543-771B-629 Sequence 205, App 11.5 5.0 20 3 US-09-543-771B-629 Sequence 202, App 11.5 5.0 20 3 US-09-081-646-743 Sequence 21, App 11.5 5.0 20 3 US-09-081-640-743 Sequence 21, App 11.5 5.0 20 3 US-09-081-640-239 Sequence 21, App 11.5 5.0 20 20 20-081-640-234 Sequence 2242, App 11.5 5.0 20 20-081-648-2242 Sequence 2242, App 2242 S	ALIGNMENN pplication US/09198452A 94 10N: Eats, R. 10N: Chlamydia pneumoniae g 10N: thoreof and uses their 10N: and treatment of infe 9710-003-99 710N WDMBER: US/09/198,452) DATE: 1998-11-24 D NOS: 6849 NOS: 6849	Query Match 69.0%; Score 13.8; DB 3; Length 20; Best Local Similarity 88.2%; Pred. No. 6.7e+02; Agence 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0; I GACCGCATAGACTTCTC 17 Agence 19 Agence 19
254 111.2 226 111.2 229 111.2 229 111.2 239 111.2 239 111.2 239 111.2 239 111.2 239 111.2 239 111.2 239 111.2 239 111.2 244 111.0 6 6 444 110.6 445 110.6 44	SULT 1 -09-198-452A-281 Sequence 2812, A Sequence 2812, A BAPLICANT: GF16 APPLICANT: GT1 TITLE OF INVENT TITLE	Query Match Best Local Simil Matches 15; C 1 GACC 1 GACC 1 GACC 2 GACC 10-007-010-48/C Sequence 48, App Patent No. 68281 GENERAL INFORMAT APPLICANT: Kem APPLICANT: Kem TITLE REPERENCE: CURRENT APPLICA CURRENT FILING NUMBER OF INVENT FILE REPERENCE: CURRENT FILING NUMBER OF INVENT SIGNORMAT FILING NUMBER OF SEQ IS SEQ ID NO 48 LENGTH: 20
00000000 0 0	RESULT US-09-: Seque Page Relation TITI TITI TITI TITI TITI TITI TITI TI	Query Best I Best L Oy Oy Db RESULT 2 US-10-00 ; Sequen ; Patent ; Patent ; GENERA ; APPLI ; ITTLE ; ITTLE ; ITTLE ; TITLE ; TOTRE ; CURRE ; CURRE ; CURRE ; SEQ IDD ; SEQ IDD

TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Antisense Oligonucleotide

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Sequence 75, Application US/09106038A
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Schatzman, Randall C.
APPLICANT: Schatzman, Randall C.
APPLICANT: Schatzman, Randall C.
TITLE OF INVENTION: DIAGNOSIS AND COMPOSITIONS FOR
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
TITLE OF INVENTION: ISPRASS;
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                              Query Match 66.0%; Score 13.2; DB 3; Length 20; Best Local Similarity 83.3%; Pred. No. 1.4e+03; Matches 15; Conservative 0; Mismatches 3; Indels
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Pred. No. 2.9e+03;
0; Mismatches 4; Indels
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COMPUTEY: NY
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTRARE: FastSED for Windows Version 2.0b
SOFTRARE: PastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,559
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 33-MAY-1997
APPLICATION NUMBER: US 08/834,497
FILING DATE: 33-MAY-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 33-MAY-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 33-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT INFORMATION:
NAME: POISSANT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08920559 Patent No. 6849399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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Best Local Similarity 78.9
Matches 15; Conservative
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STRANDEDNESS: single
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US-08-920-559-12
US-10-007-010-48
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US-08-920-559-12
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RESULT 4 US-09-106-038A-75/c

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APPLICANT: Schatzman, Randall C.
APPLICANT: Schatzman, Randall C.
APPLICANT: Tsuchihashi, Zenta
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF IRON MISREGULATION DIAGNOSIS BEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Patent No. 6007995
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FRSEESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,559
                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: Use 26, 1998
CLASSIFICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
ATTORNEY/AGENT INPORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: (760) 931-9200
TELEFAX: (760) 931-3820
TELEFAX: (760) 931-3820
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TELEFAX: (760) 931-3820
TELEFAX: LEWARTERISTICS:
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US-08-920-559-11
Sequence 11, Application US/08920559
Patent No. 6849399
GENERAL INFORMATION:
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COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
.........RR: IBM COMpatible
                                                                                                                                                                                                                2292 Faraday Avenue
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Best Local Similarity 82.4%;
Matches 14; Conservative
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-75
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STATE: CA
STATE: CA
STATE: U.S.A.
                                                                                                                                                                                                             STREET: 2292 Fe
CITY: Carlsbad
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Length 20;
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                                                                                                                                                                                                                                                                                                        Sequence 60, Application US/07799828C

Patent No. 5378602

GENERAL INFORMATION: TOTAL and APPLICANT: Mihael H. Polymeropoulos

TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE

TITLE OF INVENTION: POLYMORPHIC DNA MARKERS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lowe, Price, LeBlanc & Becker

STREET: Suite 300, 99 Canal Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60, Application US/07952277A

Patent No. 5861504

GENERAL INFORMATION:
APPLICANT: Dre. Mihael H. Polymeropoulos
APPLICANT: and Carl R. Merril
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.0%; Score 12; DB 2; Le
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5;
                                                  60.0%; Score 12; DB 2; 75.0%; Pred. No. 6.1e+03; 1ve 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/799,828C
                                                                                                                                                 1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                          1 GACCCACAGCCTATTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. MILLS
RECISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 71701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACCCCACAGCCTATTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-799-828C-60
                                                  Query Match
Best Local Similarity 75.0°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
STATE: Virginia
COUNTRY: USA
    US-07-922-723A-60
                                                                                                                                                                                                                                                              RESULT 7
US-07-799-828C-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-952-277A-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.0%; Score 12.2; DB 3; Length 20; 82.4%; Pred. No. 4.7e+03;
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US-07-922-723A-60

# Sequence 60, Application US/07922723A
# Patent No. 5369004
# GENERAL INFORMATION:
# APPLICANT: DIE. Mihael H. Polymeropoulos
# TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
# TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
# TORRESPONDENCES: 73
# CORRESPONDENCES: 73
# ADDRESSEE: Lowe, Price, LeBlanc & Becker
# STREET: Sulte 300, 99 Canal Center Plaza
# STREET: Sulte 300, 99 Canal Center Plaza
# STREET: USA
# COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                    8907-0062-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/922,723A
                     CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 13-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       ALIGNATIA PORTAL TANAMATANA PARTER POISSANT, BETANA BERTATION NUMBER: 29,462
REFERENCE DOCKET NUMBER: 8907-TELEPHONE: 650-493-555
TELEPAX: 650-493-555
TELEPAX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs LENGTH: 20 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 7170
TELECOMMUNICATION INPORMATION:
TELEPHONE: 703 684 1111
INPORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACCGCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GACAGCACAGACTICAC 18
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
27-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 82.4
Matches 14; Conservative
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TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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US-08-716-459-1/c
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APPLICANT: SIGTANSKY, David
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%; Score 12; DB 2; Length 20; Best Local Similarity 75.0%; Pred. No. 6.1e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIDENTIANO COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,637
FILING DATE: 10-MAR-1998
PRIOR APPLICATION NUMBER: 08/579,233
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/152,313
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/152,313
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/146001
TELEPHONE: 619/678-570
...urksSEE: Lowe, Price, LeBlanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA ZID:
                                                                                                                                                                        ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/952,277A
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081C
TELECOMMUNICATION INFORMATION:
TELECHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-038-637-113
; Sequence 113, Application US/09038637
; Patent No. 6235470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La JOLING STATE: CA
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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ZIP: 92037
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                                                               Query Match 60.0%; Score 12; DB 3; Length 20; Best Local Similarity 75.0%; Pred. No. 6.1e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                           1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                 ; Sequence 1, Application US/08716459
; Patent No. 5821062
                                                                                                                               1 cacccacaccciarricacia 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 205-8000
                     TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-038-637-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0182
CURRENT PELICATION NUMBER: US/09/731,457B
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOS ANGELES
COUNTRY: LOS ANGELES
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 81corgatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA:
PILING DATE: Magust 15, 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 468CT 1107
PRIOR APPLICATION DATA: 468CT 12094
CLASSIFICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 09/297,132
PILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WASTUND ATA: 31coluding application PRIOR APPLICATION NUMBER: 09/245,466
APPLICATION NUMBER: 09/297,132
PILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                        Query Match 58.0%; Score 11.6; DB 3; Best Local Similarity 77.8%; Pred. No. 9.9e+03; Matches 14; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 289, Application US/08291932A

Patent No. 5658780

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: TIBEST TRATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NP-KB
                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-09-731-4578-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GACCACATAGATCTCTAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-291-932A-289
                                                                                                                                                                      SEQ ID NO 14
LENGTH: 20
                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.0%; Score 11.8; DB 2; Length 20; Best Local Similarity 86.7%; Pred. No. 7.7e+03; Matches 13; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: yes
PRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORIGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 14, Application US/09731457B; Patent No. 6855700; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GCATAGACTICTCAG 19
                              CATAGACTTTTGAGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-731-457B-14
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APPLICANT: Akong, Michael A.
APPLICANT: Akong, Michael M.
APPLICANT: Harpold, Michael M.
APPLICANT: Velicalebi, G.
APPLICANT: Paul
TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL
TITLE OF INVENTION: PROTEIN FUNCTION USING SAME
FILE REFERENCE: 24735-51505B
CURRENT APPLICATION NUMBER: US/08/229,150
CURRENT FILING DATE: 1994-04-18
EARLIER APPLICATION NUMBER: 07/812,254
EARLIER PILING DATE: 1991-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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CTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: Oligonuclectide used for screening of products having
CTHER INFORMATION: EcorI site adjacent to initiation codon of human
US-08-229-150-4
                      Gaps
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                  1; Indels
                  Mismatches
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Job time : 100 secs
                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08229150; Patent No. 6127133; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                 7 ATAGACTICICAG 19
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                  12; Conservative
                                                                                                                                 13 ATAGAATTCTCAG 1
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LENGTH: 17
                  Matches
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APPLICANT: Akong, Anthony
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Brust, Paul
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STRATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTEN: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTEN: ALM Compatible
COMPUTEN: ALM COMPATIBLE FORM:
COMPANDED TO COMPANDED TO
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                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                  Query Match 57.0%; Score 11.4; DB 2; Length 15; Best Local Similarity 61.5%; Pred. No. 1.2e+04; Matches 8; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.4; DB 3; Length 17;
Pred. No. 1.2e+04;
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GOFWARE: FREESEQ Vereion 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,511

CLASSIFICATION: 435

CLASSIFICATION: 435

PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/244,985

FILING DATE: 20-JUN-1994
APPLICATION NUMBER: PCT/US92/11090
FILING DATE: 18-DEC-1992
APPLICATION NUMBER: 07/812,254
FILING DATE: 20-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 6362-9738

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-434-511-4/c
; Sequence 4, Application US/08434511
; Patent No. 6057114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.0%;
92.3%;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                              7 ATAGACTICICAG 19
                                                                                                                                                                                                                                                                                                                                                                                                          |: |||::|:||
1 AUGGACUUCUCAG 13
i LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-291-932A-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-434-511-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
                                                                                                                                                                                      June 9, 2006, 01:56:41 ; Search time 839 Seconds (without alignments) 292.911 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9412572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18892170 segs, 6143817638 residues
                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                        1 gaccgcatagacttctcaga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                      US-09-743-825-10
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 20
                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 577386.	Sequence 577386.		Sequence 1312885.		Sequence 1312885.	Sequence 2812, Ap	Sequence 189820,	Sequence 189920.		Sequence 1082194,	Sequence 189820,	Sequence 189920,		Seguence 1082194.	Sequence 1065181.	
SUMMARIES	αı	US-11-083-784-577386	US-11-101-244-577386	US-11-083-784-818386	US-11-083-784-1312885	US-11-101-244-818386	US-11-101-244-1312885	US-10-289-762-2812	US-11-083-784-189820	US-11-083-784-189920	US-11-083-784-511937	US-11-083-784-1082194	US-11-101-244-189820	US-11-101-244-189920	US-11-101-244-511937	US-11-101-244-1082194	US-11-083-784-1065181	US-11-083-784-1500214
	DB	14	15	14	14	15	15	7	14	14	14	14	15	15	15	15	14	14
	Query Match Length DB	19	19	19	19	19	19	20	19	19	19	19	19	19	19	19	19	19
عد	Query Match	70.0	70.0	69.0	69.0	69.0	69.0	69.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	66.0	0.99
	Score	14	14	13.8	13.8	13.8	13.8	13.8	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.2	13.2
	Result No.	-	63	ო ს	4	Ω 5	9	7	80	σ	c 10	11	12	13	c 14	15	16	17

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Gaps

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70.0%; Score 14; DB 14; Length 19; 78.6%; Pred. No. 3.6e+03; tive 3; Mismatches 0; Indels

Query Match Best Local Similarity 78.61 Matches 11; Conservative

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RESULT 2 US-11-101-244-577386

Sequence 1065181, Sequence 48, Appl Sequence 48, Appl Sequence 6652, A Sequence 66629, A Sequence 6672, A Sequence 6672, A Sequence 6672, A Sequence 6672, A Sequence 66529, A Sequence 66529, A Sequence 66529, A Sequence 66629, A	20000000000000000000000000000000000000	
21	11 US-10-310-914A-1316661 14 US-11-083-784-36613 14 US-11-083-784-92624 14 US-11-083-784-928551 14 US-11-083-784-928551 14 US-11-083-784-1267201 14 US-11-083-784-1324219 14 US-11-083-784-1324219 14 US-11-083-784-1324219 14 US-11-083-784-1324219 15 US-11-101-244-928451 15 US-11-101-244-928550 15 US-11-101-244-928551	ALIGNMENTS ation US/11083784 1245475A1 Inc. Anastasia Angela in William William William William Stephen nctional and Hyperfunctional siRNA NBER: US/11/083,784 2005-03-18 ER: US/10/714,333 3-11-14 1591911
66666666666666666666666666666666666666	12.8 64.0 199 12	84-577386 577386, Applic 577386, Applic ON No. 220050 NFORMATION: T: Exprolds, T: E
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 00 0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-11-083-78 SEQUENCE 5 SEQUENCE 1N SEQUENCE 1N SEQUENCE 1N SEPLICANT SEPLICANT SEPLICANT SEPLICANT SEPLICANT SEPLICANT SEPLICANT SEPLICANT SERVER

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US-11-083-784-1312885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-083-784-818386/C

i Sequence 818386, Application US/11083784

j Publication No. US20050245475A1

i GENERAL INFORMATION:
    APPLICANT: Diarmacon, Inc.
    APPLICANT: Revorova, Anstasia
    APPLICANT: Revorova, Anstasia
    APPLICANT: Revorova, Anstasia
    APPLICANT: Beak, Devin
    APPLICANT: Beak, Devin
    APPLICANT: Beak, Devin
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    TITLE OF INVENTION WURBER: US/11/083, 784
    CURRENT APPLICATION NUMBER: US/10/714,333
    PRIOR APPLICATION NUMBER: 60/502,050
    PRIOR PILING DATE: 2003-10-11
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2002-11-14
    NUMBER: OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 81386
    LENGTH: 19
                                     GENERAL INFORMATION

APPLICANT: Dharmacon, Inc.
APPLICANT: Reyrolds, Ansteasia
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILER REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
SOFTWARE: PROPRICATION NUMBER: 60/426,137
RIOR FILING DATE: 2002-11-14
SOFTWARE: PROPRICATY
SEQ ID NOS: 1591911
SEQ ID NO 577386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14; DB 15; Length 19;
Pred. No. 3.6e+03;
3; Mismatches 0; Indels
Sequence 577386, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 78.6°
Matches 11, Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Homo Bapiens
US-11-101-244-577386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-083-784-818386
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RESULT 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 13.8; DB 15; Length 19; 88.2%; Pred. No. 4.6e+03; ive 0; Mismatches 2; Indels
                                                             GENERAL INCOMPATION:

APPLICANT: Khorova, Anastasia
APPLICANT: Kryolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Asrablal, William
APPLICANT: Asrablal, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
FRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1312885
LEMOTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 818386
TENNORTH OF SEQ ID NOS: 1591911
Sequence 1312885, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 818386, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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Best Local Similarity 88.2
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-083-784-1312885
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US-11-101-244-818386
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Matches 12; Conserv
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                                                                                   APPLICANT: Scatinge, Stephen
ITILB OF INVENTION: Functional and Hyperfunctional sirNA
ITILB REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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APPLICANT: Characton, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE OF INVENTION: Punctional and Hyperfunctional
FILE REPERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
FRIOR PELICATION NUMBER: US/10/714,333
FRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 189920
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Best Local Similarity 73.3%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 189920, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
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... Sequence 511937, Application US/11083784
... Publication No. US205050245475A1
... GENERAL INFORMATION:
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Best Local Similarity 73.3
Matches 11, Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-189820
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US-11-083-784-189920
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Ouery Match 69.0%; Score 13.8; DB 7; Length 20; Best Local Similarity 89.2%; Pred. No. 4.6e+03; Matches 15; Conservative 0; Mismatches 2; Indel8
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2812, Application US/10289762
Publication No. US20040006218A1
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1312885
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Publication No. US20050246794A1
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US-11-101-244-511937/c
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Pred. No. 7.6e+03;
4; Mismatches 1; Indels (
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marahall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SQUING PRIOR SEQ ID NOS: 1591911
SEQ ID NO 511937
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PUBLICALION OF USZUDSUASALA |
| PUBLICANT: Dharmacon, Inc. |
| APPLICANT: CANTON Anastasia |
| APPLICANT: Khvorova, Anastasia |
| APPLICANT: Khvorova, Anastasia |
| APPLICANT: Reyrolds, Angela |
| APPLICANT: Leake, Devin |
| APPLICANT: Leake, Devin |
| APPLICANT: Carringe, Stephen |
| TILLE OF INVENTION: Punctional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| TILLE OF INVENTION: Punctional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| CURRENT FILING DATE: 2005-03-18 |
| PRIOR APPLICATION NUMBER: US/11/083,784 |
| PRIOR PILING DATE: 2003-11-14 |
| PRIOR APPLICATION NUMBER: 60/502,050 |
| PRIOR FILING DATE: 2003-09-10 |
| PRIOR FILING DATE: 2003-11-14 |
| NUMBER OF SEQ ID NOS: 1591911 |
| SOFTWARE: PROPRIETARY |
| LENGTH: 19
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Publication No. US20050245475A1
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US-11-101-244-189820
; Sequence 189820, Application US/11101244
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CAUCGACUUCUCAGA 15
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Best Local Similarity 66.7
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-511937
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; ORGANISM: Homo sapiens
US-11-083-784-1082194
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Best Local Similarity
Matches 14; Conserva
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GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhorova, Anastasia
APPLICANT: Rhorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: FUNCTIONAL
FILE REFERENCE: 13499US
CURRENT PELLING DATE: 2005-04-07
FRIOR RAPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PLILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-01-114
NUMBER OF SEQ ID NOS: 1591911
SSOTUARE: PROPRIECATY
ILENGTH: 19
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Barahall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 1349908
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PLILING DATE: 2005-04-07
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-10-10-04
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SCOTTWARE: Proprietary
SEQ ID NO 189920
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Pred. No. 7.6e+03;
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1 Similarity 73.3%; Pred. No. 7.6e+03;
11; Conservative 3; Mismatches 1;
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Sequence 189920, Application US/11101244
Publication No. US20050246/94A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.0%;
Best Local Similarity 73.3%;
Matches 11; Conservative
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US-11-101-244-189820
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Responds, Angela
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
TILE APPLICANT: Marshall, William
APPLICANT: 2010-04-07
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
SOFTWARE: PROPRIET 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 511937
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1082194, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INPORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Stephen
| APPLICANT: Marshall, William
| APPLICANT: Reynolds, Stephen
| TILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: 06/502.050
| PRIOR APPLICATION NUMBER: 60/426,137
| PRIOR PILING DATE: 2003-09-10
| PRIOR PILING DATE: 2003-01-14
| SOFTWARE: PROPICEATY
| SEQ ID NOS: 1591911
| SEQ ID NO 1082194
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Best Local Similarity 66.74
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-511937
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CORGANISM: Homo sapiens
US-11-101-244-1082194
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US-11-101-244-1082194
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Search completed: June 9, 2006, 02:12:17 Job time : 840 secs Colosn) Midle Scot Silly

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20 GACCTCACAGACGACACAGA 1
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Best Local Similarity 75.0%;
Matches 15; Conservative (
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        9999777979799999
RESULT 2
US-10-514-776-214/c
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SEQ ID NO 45
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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201, App
18, Appl
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                                                June 9, 2006, 01:58:21 ; Search time 23 Seconds (without alignments) 110.368 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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Sequence 38,
Sequence 993,
Sequence 5435
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      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-514-776-214
US-11-251-465-365
US-11-251-465-38
US-11-293-637-993
US-11-293-637-993
US-11-251-465-371
US-10-511-937-993
US-11-251-465-371
US-10-469-938A-158
US-10-469-938A-158
US-10-469-938A-158
US-10-469-938A-158
US-11-251-465-201
US-11-251-465-201
US-11-251-465-201
US-11-261-461-256
US-11-265-761-268
US-11-265-761-268
US-11-265-761-268
US-10-474-853-41
US-10-651-832-21
US-10-651-832-21
                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-11-110-361A-84
                                                                                                                                      253354 seqs, 63461778 residues
                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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10, Appl
10, Appl
32, Appl
25, Appl
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: Primer
OTHER INFORMATION: Primer
                                                                                                                                                                      Sequence
                                                                                                                                                                                                          Sequence
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Pred. No. 4.18+02;
; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Application US/11189279

Sequence 45, Application US/11189279

Publication No. US20060115829A1

GENERAL INFORMATION:

APPLICANT: MAO, LI

APPLICANT: WANG, JIE

APPLICANT: LUO, WANG

TILLE OF INVENTION: A METHOD OF TREATING CANCER

FILE REFERENCE: UTXC:875US

CURRENT FILING DATE: 2005-07-26

PRIOR APPLICATION NUMBER: 60/598,554

PRIOR APPLICATION NUMBER: 60/598,554

PRIOR PILING DATE: 2004-08-03

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PATENTING DATE: 2005-07-06

SOFTWARE: PATENTING DATE: 2.1
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sysmex Corporation
TITLE OF INVENTION: CK primer
FILE REFERENCE: GP03-1006PCT
CURRENT APPLICATION NUMBER: US/10/514,776
CURRENT FILING DATE: 2004-11-19
PRIOR APPLICATION NUMBER: JP P2002-145689
PRIOR PLILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: JP P2002-175271
PRIOR PILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 214, Application US/10514776; Publication No. US20060094008A1; GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-12-20
PRIOR PELIANG NUMBER: PCT/AU01/00729
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 51
SEG ID NO 38
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 993, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
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CRGANISM: Homo mapiens
US-10-511-937-993
                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-264-558-38
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| Publication No. US20060094061A1 |
| Sequence 365, Application No. US20060094061A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Tomme, Peter |
| APPLICANT: Information: Useful in The Treatment of Joint Degenerative And |
| TITLE OF INVENTION: Inflammatory Diseases |
| TITLE OF INVENTION: Inflammatory Diseases |
| TITLE OF INVENTION: Inflammatory Diseases |
| TITLE OF INVENTION: UNMER: US/11/251,465 |
| TITLE OF INVENTION NUMBER: US/11/251,465 |
| OURRENT APPLICATION NUMBER: US/11/251,465 |
| WRIOR APPLICATION NUMBER: 2004-10-15 |
| NUMBER OF SEQ ID NOS: 880 |
| SOFTWARE: Patentin version 3.3 |
| LENGTH: 19
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Pred. No. 4.8e+03;
0; Mismatches 5; Indels
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Publication No. US20060088913A1
GENERAL INFORMATION:
APPLICANT: Blacon Limited
APPLICANT: Mullace, Robyn H
APPLICANT: Mullace, Robyn H
APPLICANT: Mullace, Robyn H
APPLICANT: Mullace, Samuel F
APPLICANT: Dibbens, Leanne M
TITLE OF INVENTION: MUTATION ASSOCIATED WITH EPILEPSY
FILE REFERENCE: 1386/10/2
CURRENT FILING DATE: 2005-11-01
PRIOR APPLICATION NUMBER: US/11/264,558
                                                                                                                                                                                                               ; OTHER INFORMATION: Designed DNA based on CK18
US-10-514-776-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Knock-down target sequence US-11-251-465-365
PRIOR APPLICATION NUMBER: JP P2002-199759
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 474
SEQTYARE: PatentIn version 3.1
SEQ ID NO 214
LENGTH: 19
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Best Local Similarity 72.2%;
Matches 13; Conservative (
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                                                                                                                                                                   ORGANISM: Artificial
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US-11-264-558-38/c
                                                                                                                                               TYPE: DNA
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APPLICANT: Mohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Worris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: PGT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR PELING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Query Match 50.0%; Score 10; DB 7; Length 20; Best Local Similarity 100.0%; Pred. No. 4.8e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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49.0%; Score 9.8; DB 6;
Best Local Similarity 84.6%; Pred. No. 6.2e+03;
Matches 11; Conservative 0; Mismatches 2.
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US-211-293-697-5435
Sequence 5435, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILLS REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILLING DATE: 2005-12-05
PRIOR FILLING DATE: 2005-12-05
PRIOR FILLING DATE: 2005-03-28
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Gaps
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Sequence 158, Application US/10469938A

Fublication No. US20060105329A1

GRUERAL INFORMATION:
TITLE OF INVENTION: Gene Panel for Genes Involving Liver Regeneration
FILE REFERENCE: B868AYOP1331

CURRENT APPLICATION NUMBER: US/10/469, 938A

CURRENT FILING DATE: 2003-09-05

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 192

SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Moddward; Robert
APPLICANT: IV, Ngoc
APPLICANT: IV, Ngoc
APPLICANT: Prentice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US,10/511,937
CURRENT PILING DATE: 2004-01-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US, 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOOFTWARE PATENTIN OF SECON OF 
                                                                                                                                                                                                                                                                                                                                     Query Match
46.0%; Score 9.2; DB 7; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+04;
                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 704, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Noodward, Robert
              SOFTWARE: PatentIn version 3.3
                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 78.6%;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-511-937-704
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                                                SEQ ID NO 371
LENGTH: 19
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Fublication No. US20060094061A1

GENERAL INFORMATION:

APPLICANT: Brys, Reginald

APPLICANT: Towne, Peter

APPLICANT: Klaasen, Hubertus

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Unitation of Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION: Same, Useful In The Treatment of Joint Degenerative And

TITLE OF INVENTION NUMBER: US/11/251,465

CURRENT APPLICATION NUMBER: 60/619,384

PRIOR FILING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880
                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized US-11-293-697-5435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/11247332

Fublication No. US20060094667A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Hideki

TITLE OF INVENTION: Medicines
TITLE OF INVENTION: Medicines
FILE REFERENCE: Q76132

CURRENT APPLICATION NUMBER: US/11/247,332

CURRENT FILING DATE: 2005-10-12

FRIOR APPLICATION NUMBER: US/10/451,926

FRIOR APPLICATION NUMBER: PCT/JP01/11348

FRIOR FILING DATE: 2001-12-25

FRIOR FILING DATE: 2001-12-25

FRIOR FILING DATE: 2000-12-28

NUMBER OF SRQ ID NOS: 5

SRQ ID NO 2

LENGTH: 20
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48.0%; Score 9.6; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 12; Conservative 0; Mismatches 4; Indels
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48.0%; Score 9.6; DB 7; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCCTAGCCCTCTCA 16
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5435
LENGTH: 18
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US-11-251-465-371/c
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; OTHER INFORMATION: Description of Artificial Sequence: sense upstream vector Primer; OTHER INFORMATION: ADJ014
US-10-521-008-6
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| Publication No. US20060099175A1
| GENERAL INFORMATION:
| APPLICANT: Van Den Hazel, Bart
| APPLICANT: Van Den Hazel, Bart
| APPLICANT: Andersen, Kim V.
| APPLICANT: Mygaard, Frank B.
| APPLICANT: Mygaard, Frank B.
| APPLICANT: Nygaard, Frank B.
| APPLICANT: Nygaard, Frank B.
| APPLICANT: Nygaard, Frank B.
| APPLICANT: NowEMER: US/10/521,008
| CURRENT APPLICANTION NUMBER: US/10/521,008
| CURRENT FILING DATE: 2005-01-03
| PRIOR FILING DATE: 2003-06-23
| NUMBER OF SEQ ID NOS: 13
| SEQ ID NOS: 13
| SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Omnen van, Garrit-Jan B.
APPLICANT: Omnen van, Garrit-Jan B.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Deutekom van, John C.T.
APPLICANT: Deutekom van, John C.T.
APPLICANT: Aartsma-Rus, Annemieke T.
APPLICANT: Aartsma-Rus, Annemieke T.
TITLE OF INVENTION: interfering with the secondary RNA structure FILE REPRENCE: P639170500
CURRENT APPLICATION NUMBER: US/11/233,507
CURRENT PILING DATE: 2006-03-21
PRIOR PILING DATE: 2004-03-22
PRIOR PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 18
LENGTH: 18
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US-11-233-507-18
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44.0%; Score 8.8; DB 7; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 8; Conservative 2; Mismatches 2; Indels
                                                                               45.0%; Score 9; DB 7; Length 19; 100.0%; Pred. No. 1.6e+04; Live 0; Mismatches 0; Indels
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; Sequence 18, Application US/11233507
; Publication No. US2006009616A1
; GENERAL INFORMATION:
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                                                                                                                                                       Conservative
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                                              Query Match
Best Local Similarity
              US-11-251-465-201
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vs-squence 201, Application US/11251465
publication No. US20060094061A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Inflammatory Diseases
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT PILIG DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR PILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE PATENTIN VERSION 3.3
SEQ ID NO 201
LENGTH: 19
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US-10-469-938A-63
i Sequence 6.3, Application US/10469938A
j Publication No. US20060105329A1
j GENERAL INFORMATION:
i APPLICANT: Ajinomoto Co., Inc.
i TILLE OF INVENTION: Gene Panel for Genes Involving Liver Regeneration
f FILE REFERENCE: B866AYOF133
i CURRENT APPLICATION NUMBER: US/10/469,938A
j CURRENT APILICATION NUMBER: JP 2001-070940
j PRIOR FILING DATE: 2003-09-05
j PRIOR FILING DATE: 2001-03-13
j NUMBER OF SEQ ID NOS: 192
j SOFFWARE: PatentIn Ver. 2.0
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                                                                TYPE: DNA ORGANISM: Artificial Sequence CATURE: PEATURE: OTHER INFORMATION: Description of Artificial Sequence: primer US-10-469-938A-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: primer US-10-469-938A-63
                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                              Query Match
46.0%; Score 9.2; DB 6; Length 20
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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SEQ ID NO 158
LENGTH: 20
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LENGTH: 18
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Query Match

44.0%; Score 8.8; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels
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44.0%; Score 8.8; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     RESULT 15
US-10-524-399-14
Sequence 14, Application US/10524399
Sequence 14, Application US/10524399
FUDICATION NO. US20060099591A1
GENERAL INFORMATION:
APPLICANT: KRAUER, Addreas
APPLICANT: RAULF, Friedrich
APPLICANT: RAULF, Friedrich
APPLICANT: SCHERR, Addreas
ITLE OP INVENTION Diagnosis of chronic rejection
FILE REFERENCE: 4-32608A
CURRENT APPLICATION NUMBER: US/10/524,399
CURRENT FILING DATE: 2005-02-11
FRIOR FILING DATE: 2005-02-11
FRIOR RILING DATE: 2005-02-11
FRIOR FILING DATE: 2005-03-11
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19 ATAGACCTCCCA 8
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Search completed: June 9, 2006, 02:12:47 Job time : 24 Becs

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